

## SEARCH REQUEST FORM

Requestor's  
Name: Sally Teng Serial  
Number: 08/426,509  
Date: 1/27/97 Phone: 308-4230 Art Unit: 1812

**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please Search

① Amino acids ~~48 to 111~~, <sup>SH<sub>3</sub></sup> kinase <sup>SH<sub>2</sub></sup> 233-478, + 122-196  
of SEQ ID NO: 2

② Amino acids ~~25 to 109~~, <sup>SH<sub>2</sub></sup> 296-375, + 192-234  
+ 424 to 659 of SEQ ID NO: 4 <sup>kinase</sup>

③ Amino acids ~~122 to 201~~, <sup>SH<sub>3</sub></sup> 54 to 112, <sup>SH<sub>2</sub></sup> 247 to 486  
of SEQ ID NO: 6

④ Amino acids 493-507; of SEQ ID NO: 2

⑤ . . . 66 C-675 . . . 4

**STAFF USE ONLY**

1-552

Date completed:	Search Site	Vendors
02-04-97	STIC	IG
Searcher: <u>Beverly 04-29-99</u>	CM-1	STN
Terminal time: <u>15</u>	Pre-S	Dialog
Elapsed time:		
CPU time:		APS
Total time: <u>27</u>	N.A. Sequence	Geninfo
Number of Searches:	A.A. Sequence	SDC
Number of Databases: <u>1</u>	Structure	DARC/Questel
	Bibliographic	Other <u>MF</u>

FT /note= "replaces wild-type TLLSAL"  
FT Misc\_difference 361  
FT /label= Met, Trp, Ala, Asn, Asp, Cys, Gln, Glu,  
FT Gly, His, Ile, Lys, Phe, Pro, Ser, Thr,  
FT Tyr, Val  
FT /note= "pref. Met (claim 3)"  
PN WO9527053-A1.  
PD 12-OCT-1995.  
PF 29-APR-1994; U04703.  
PR 31-MAR-1994; US-221171.  
PA (UYPE-) UNIV PENNSYLVANIA.  
PI Cooperman BS, Rubin H, Schechter N, Wang ZM;  
DR WPI; 95-366158/47.  
PT Analogues of human alpha-1-anti:chymotrypsin with increased  
PT inhibitory activity - useful for treating lung inflammation etc  
PT also related nucleic acid, vectors and transformed cells.  
PS Claim 8; Fig 1A-1E; 54pp; English.  
CC Analogues of wild-type alpha-1-antichymotrypsin (a1-ACT) (R83101  
CC may be produced, by recombinant DNA methods, in which amino acid  
CC 356-361 of the mature protein are replaced by other residues (e.  
CC see R83102-03), and optionally contain a modified N-terminal  
CC extension (see also R83104-05). The N-terminal extensions M-A-S  
CC or A-S on the wild-type and analogue proteins enable direct  
CC expression of stable monomers. The wild-type protein and analog  
CC are used as chymase inhibitors and in the treatment and preventi  
CC of blood clots, reperfusion injury and lung inflammation, the  
CC latter caused by acid inhalation (from stomach contents or smoke  
CC or infection by a Gram-negative bacterium (e.g. *Pseudomonas* or  
CC *Escherichia*). The analogues are prepared by protein engineering  
CC techniques, and are 4-fold more efficient at inhibiting chymase  
CC than the wild-type protein.  
SQ Sequence 401 AA;

Query Match 22.8%; Score 66; DB 16; Length 401;  
Best Local Similarity 27.3%; Pred. No. 3.89e+01;  
Matches 6; Conservative 10; Mismatches 5; Indels 1; Gaps 1

Db 128 ldrfiedakrlygsea-fatdf 148  
| :: ::|::|::| | ::  
Gy 213 LAQYDSDNSKIKIYGSQPNFHNQY 234

Search completed: Mon Feb 3 17:04:53 1997  
Job time : 8 secs.

\*\*\*\*\*  
MAPA (TM)  
\*\*\*\*\*

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:04:10 1997; MasPar time 3.45 Seconds  
320.264 Million cell updates/sec

Tahular output not generated

Title: >US-08-426-509-4  
Description: (192-234) from US08426509.pep (3 of 5)  
Perfect Score: 290  
Sequence: 1 AQYDNESKKNYGSQPPSSSTS LAQYDSNSKKIYGSQPNFNMQY 43

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:anni 2:ann2 3:ann3 4:unanni 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 31.496; Variance 62.651; scale 0.503

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	80	27.6	473	14	S61428	late embryogenesis a	3.31e-01		
2	77	26.6	458	9	S33520	Lea protein - soybea	8.66e-01		
3	77	26.6	655	5	A55726	RNA-binding protein	8.66e-01		
4	77	26.6	656	5	A49358	RNA-binding protein	8.66e-01		
5	76	26.2	2710	8	AJ7052	toxin A - Clostridiu	1.19e+00		
6	76	26.2	2710	8	S08638	toxin A - Clostridiu	1.19e+00		
7	74	25.5	870	8	S27514	mosquitocidal toxin	2.22e+00		
8	72	24.8	462	13	S33798	FUS-CHOP mutant fusi	4.11e+00		
9	72	24.8	526	5	S33799	RNA-binding protein	4.11e+00		
10	70	24.1	286	9	S32480	hypothetical protein	7.52e+00		
11	70	24.1	1538	3	RGBYS3	regulatory protein S	7.52e+00		
12	70	24.1	1986	10	S28353	probable polyketide	7.52e+00		
13	69	23.8	173	8	S38231	hypothetical protein	1.01e+01		
14	69	23.8	774	3	QRECFA	iron(III) dicitrate	1.01e+01		
15	68	23.4	213	4	S26055	2-dehydro-3-deoxypho	1.36e+01		
16	68	23.4	328	4	S16300	UDPglucose 4-epimera	1.36e+01		
17	68	23.4	396	10	S58223	LSR1 protein - yeast	1.36e+01		
18	68	23.4	396	10	S61136	probable transcripti	1.36e+01		
19	68	23.4	573	12	S20710	hypothetical protein	1.36e+01		
20	68	23.4	1394	10	A29637	position-specific an	1.36e+01		
21	67	23.1	231	8	F64120	phosphate regulon tr	1.83e+01		
22	67	23.1	316	9	S58719	hypothetical protein	1.83e+01		
23	67	23.1	439	9	A36911	glutamine synthetase	1.83e+01		
24	67	23.1	664	10	S53037	PLB1 protein - yeast	1.83e+01		
25	67	23.1	889	10	S50934	hypothetical protein	1.83e+01		
26	67	23.1	1196	14	S35994	XP-G-related protein	1.83e+01		
27	66	22.8	288	6	I36848	A8R protein - variol	2.44e+01		
28	66	22.8	320	10	S09208	chorion protein s36	2.44e+01		
29	66	22.8	433	2	ITHUC	alpha-1-antichymotry	2.44e+01		
30	66	22.8	505	10	S44647	f42h10.1 protein - C	2.44e+01		
31	66	22.8	930	10	D37271	A-alpha Z 4 protein	2.44e+01		
32	66	22.8	1094	9	S49313	protein kinase - sli	2.44e+01		
33	66	22.8	1094	9	S52076	protein kinase - sli	2.44e+01		
34	66	22.8	1146	10	S46837	hypothetical protein	2.44e+01		
35	65	22.4	107	4	B60754	glucan 1,4-alpha-glu	3.25e+01		
36	65	22.4	131	7	JC1369	hypothetical 14.2K p	3.25e+01		

37	65	22.4	270	8	H64248	hypothetical protein	3.25e+01
38	65	22.4	657	4	A64079	2',3'-cyclic-nucleot	3.25e+01
39	65	22.4	1468	12	A44345	nucleoporin - rat	3.25e+01
40	64	22.1	125	10	S53086	ND3 protein - jelly	4.32e+01
41	64	22.1	295	13	S36174	RNA binding protein/	4.32e+01
42	64	22.1	330	14	J02262	Polygalacturonase in	4.32e+01
43	64	22.1	397	1	XNECY	tyrosine transaminas	4.32e+01
44	64	22.1	459	6	J02345	major capsid protein	4.32e+01
45	64	22.1	877	9	S58824	hypothetical protein	4.32e+01

### ALIGNMENTS

RESULT 1

ENTRY S61428 #type complete

TITLE late embryogenesis abundant protein (clone pGMPM10) - soybean

ORGANISM #formal\_name Glycine Max #common\_name soybean

DATE 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 01-Mar-1996

ACCESSIONS S61428

REFERENCE S61428

#authors Chow, T.; Hsing, Y.C.; Chen, Z.

#submission submitted to the EMBL Data Library, October 1993

#description cDNA sequences for a soybean seed maturation polypeptide gene family.

#accession S61428

##status preliminary

##residues 1-473 ##label CHO

##cross-references EMBL:U02966

SUMMARY #length 473 #molecular-weight 50982 #checksum 278

Query Match 27.6%; Score 80; DB 14; Length 473;  
 Best Local Similarity 21.6%; Pred. No. 3.31e-01;  
 Matches 8; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Db 195 dyatqktdydasdatdaakktdyaqktdyaseas 231  
 :| : |::|:: :| : | |::|:::  
 Qy 193 QYDNE SKKNYGSQPPSSSTS LAQYDSNSKKIYGSQPN 229

RESULT 2

ENTRY S33520 #type complete

TITLE Lea protein - soybean

ORGANISM #formal\_name Glycine Max #common\_name soybean

DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

ACCESSIONS S33520

REFERENCE S33520

#authors Chow, T.; Hsing, Y.C.; Chen, Z.

#submission submitted to the EMBL Data Library, June 1993

#description cDNA sequences for a soybean seed maturation polypeptide gene family.

#accession S33520

##status preliminary

##molecule\_type mRNA

##residues 1-458 ##label CHO

##cross-references EMBL:Z22872

SUMMARY #length 458 #molecular-weight 49399 #checksum 5605

Query Match 26.6%; Score 77; DB 9; Length 458;  
 Best Local Similarity 22.2%; Pred. No. 8.66e-01;  
 Matches 8; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Db 181 dyatqktdydasdatdaakktdyaqktdyasd 216  
 :| : |::|:: :| : | |::|:::  
 Qy 193 QYDNE SKKNYGSQPPSSSTS LAQYDSNSKKIYGSQPN 228

Search completed: Mon Feb 3 17:00:21 1997

Job time : 10 secs.

For more information, contact the Office of the Vice President for Research and the Office of the Vice President for Student Affairs.

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:59:28 1997; MasPar time 4.51 Seconds  
456,034 Million cell updates/sec

Tabular output not generated.

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 37.725; Variance 82.158; scale 0.459

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

17

Result	Query						
No.	Score	Match	Length	DB	ID	Description	Pred. No.
<hr/>							
1	325	56.1	659	11	I37212	Bruton agammaglobuli	8.36e-39
2	325	56.1	659	11	S28912	protein-tyrosine kin	8.36e-39
3	324	56.0	659	12	B45184	B cell progenitor ki	1.26e-38
4	324	56.0	660	12	JN0471	protein-tyrosine kin	1.26e-38
5	319	55.1	442	11	A45184	B cell progenitor ki	9.71e-38
6	311	53.7	620	4	S33253	protein-tyrosine kin	2.54e-36
7	307	53.0	619	4	JN0472	protein-tyrosine kin	1.29e-35
8	307	53.0	619	4	A47333	T-cell-specific tyro	1.29e-35
9	307	53.0	625	4	A43030	protein-tyrosine kin	1.29e-35
10	300	51.8	527	12	A55631	protein-tyrosine kin	2.21e-34

11	291	50.3	527	4	S1J763	protein-tyrosine kin	8.42e-33
12	291	50.3	602	4	JU0215	tyrosine kinase, tec	8.42e-33
13	291	50.3	608	4	JU0227	protein-tyrosine kin	8.42e-33
14	291	50.3	630	4	JU0228	protein tyrosine kin	8.42e-33
15	254	43.9	590	1	TVFFDS	protein-tyrosine kin	2.23e-26
16	166	28.7	499	4	A40092	protein-tyrosine kin	8.32e-12
17	166	28.7	505	1	TVHUHC	protein-tyrosine kin	8.32e-12
18	162	28.0	517	4	A4J807	protein-tyrosine kin	3.53e-11
19	161	27.8	537	4	A45501	protein-tyrosine kin	5.05e-11
20	160	27.6	517	12	S24547	protein-tyrosine kin	7.24e-11
21	159	27.5	503	4	JQ1321	protein-tyrosine kin	1.04e-10
22	159	27.5	503	1	TVMSHC	protein-tyrosine kin	1.04e-10
23	158	27.3	528	1	TVFVG9	protein-tyrosine kin	1.48e-10
24	158	27.3	541	1	TVCHYS	protein-tyrosine kin	1.48e-10
25	158	27.3	543	1	TVHUY5	protein-tyrosine kin	1.48e-10
26	158	27.3	557	10	A00629	protein-tyrosine kin	1.48e-10
27	157	27.1	541	4	A43610	protein-tyrosine kin	2.12e-10
28	157	27.1	541	12	S31645	protein-tyrosine kin	2.12e-10
29	157	27.1	542	1	TVHUSC	protein-tyrosine kin	2.12e-10
30	156	26.9	529	1	TVHUFR	protein-tyrosine kin	3.03e-10
31	155	26.8	526	1	TVFV60	protein-tyrosine kin	4.32e-10
32	155	26.8	533	1	TVCHS	protein-tyrosine kin	4.32e-10
33	155	26.8	539	11	B49114	protein-tyrosine kin	4.32e-10
34	155	26.8	557	1	TVFV52	protein-tyrosine kin	4.32e-10
35	155	26.8	587	1	TVFVPR	protein-tyrosine kin	4.32e-10
36	154	26.6	663	1	TVMVRR	protein-tyrosine kin	6.16e-10
37	154	26.6	1290	11	A36466	1-phosphatidylinosit	6.16e-10
38	154	26.6	1290	12	A31317	1-phosphatidylinosit	6.16e-10
39	154	26.6	1291	12	S00666	1-phosphatidylinosit	6.16e-10
40	153	26.4	536	4	S33569	protein-tyrosine kin	8.79e-10
41	153	26.4	981	1	F0HVG0	gag-abl polyprotein	8.79e-10
42	153	26.4	1123	4	A39962	kinase-related trans	8.79e-10
43	153	26.4	1130	1	TVHUA	protein-tyrosine kin	8.79e-10
44	152	26.3	526	1	TVFVR	protein-tyrosine kin	1.25e-09
45	152	26.3	568	1	TVFV51	protein-tyrosine kin	1.25e-09

## ALIGNMENTS

RESULT 1

ENTRY I37212 #type complete

TITLE Bruton agammaglobulinemia tyrosine kinase - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Mar-1996

ACCESSIONS I37212

REFERENCE I37212

#authors Ohta, Y.; Haire, R.N.; Litman, R.T.; Fu, S.M.; Nelson, R.P.; Kratz, J.; Kornfeld, S.J.; de la Morena, M.; Good, R.A.; Litman, G.W.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9062-9066

#title Genomic organization and structure of Bruton agammaglobulinemia tyrosine kinase: localization of mutations associated with varied clinical presentations and course in X chromosome-linked agammaglobulinemia.

#cross-references MUID:94377492

#accession I37212

##status preliminary

##molecule\_type DNA

##residues 1-659 ##label RES

##cross-references EMBL:U10087; NID:g517436; CDS\_PID:g517438

##note only intron-exon junctions are shown

GENETICS

#gene GDB:BTK; AGMX1; IMD1

##cross-references GDB:G00-120-542

#gen position Xq21.33-a22

#introns 47/3; 80/3; 103/3; 131/1; 174/1; 196/3; 259/2; 280/2; 298/3;  
325/2; 368/1; 393/1; 450/2; 522/3; 544/2; 584/1; 636/3  
SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 56.1%; Score 325; DB 11; Length 659;  
Best Local Similarity 48.8%; Pred. No. 8.36e-39;  
Matches 39; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhmtrsqaeqllkqegkeggfivrdsskagkytvsvfakstgdpqgvirhyvvctp 340  
||: ::||:||:||:|| | ||||:||:||:|| | :||:||:||: | | :|| | : :  
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMYTDSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqyylaekhlfstipelin 360  
:: ||||: | :|| ||:  
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 2

ENTRY S28912 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) atk - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change  
01-Dec-1995  
ACCESSIONS S28912  
REFERENCE S28912  
#authors Vetrici, D.; Vorechovsky, I.; Sideras, P.; Holland, J.;  
Davies, A.; Flinter, F.; Hammarstroem, L.; Kinnon, C.;  
Levinsky, R.; Bobrow, M.; Smith, C.I.E.; Bentley, D.R.  
#journal Nature (1993) 361:226-233  
#title The gene involved in X-linked agammaglobulinaemia is a member  
of the src family of protein-tyrosine kinases.  
#accession S28912  
##status preliminary  
##molecule\_type mRNA  
##residues 1-659 ##label VET  
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
homology  
KEYWORDS phosphotransferase  
FEATURE  
221-269 #domain SH3 homology #label SH3\  
281-377 #domain SH2 homology #label SH2\  
400-658 #domain protein kinase homology #label KIN  
SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 56.1%; Score 325; DB 11; Length 659;  
Best Local Similarity 48.8%; Pred. No. 8.36e-39;  
Matches 39; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhmtrsqaeqllkqegkeggfivrdsskagkytvsvfakstgdpqgvirhyvvctp 340  
||: ::||:||:||:|| | ||||:||:||:|| | :||:||:||: | | :|| | : :  
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMYTDSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqyylaekhlfstipelin 360  
:: ||||: | :|| ||:  
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 3

ENTRY B45184 #type complete  
TITLE B cell progenitor kinase, BPK=cytoplasmic tyrosine kinase -  
mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change  
12-May-1995  
ACCESSIONS B45184  
REFERENCE A45184

**#authors** Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.;  
 Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.;  
 Mohandas, T.; Quan, S.; Belmont, J.W.; Cooper, M.D.;  
 Conley, M.E.; Witte, O.N.  
**#journal** Cell (1993) 72:279-290  
**#title** Deficient expression of a B cell cytoplasmic tyrosine kinase  
 in human X-linked agammaglobulinemia.  
**#cross-references** MUID:93145329  
**#accession** B45184  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type nucleic acid  
 ##residues 1-659 ##label TSU  
 ##cross-references NCBIP:123834  
 ##experimental\_source 70z/3 pre-B cell line  
 ##note sequence extracted from NCBI backbone  
**CLASSIFICATION** #superfamily SH3 homology; protein kinase homology; SH2  
 homology  
**FEATURE**  
 221-269 #domain SH3 homology ##label SH3\  
 281-377 #domain SH2 homology ##label SH2\  
 400-658 #domain protein kinase homology ##label KIN  
**SUMMARY** #length 659 #molecular-weight 76326 #checksum 9917  
  
 Query Match 56.0%; Score 324; DB 12; Length 659;  
 Best Local Similarity 47.5%; Pred. No. 1.26e-38;  
 Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;  
  
**Db** 281 *wyskhmttrsqaeqllkqegkeggfivrdsskagkytvsvfakstgepqqvirhyvvctsp* 340  
 ||:: :::: ||:: ||:: || ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:  
**Qy** 296 *WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMYTVSLFSKAVNDKKGTVKHYHVHTNA* 355  
  
**Db** 341 *qsqyylaekhlfstipelin* 360  
 :: ||:: ||:: ||:: ||:  
**Qy** 356 *ENKLYLAENYCFDSIPKLIH* 375  
  
**RESULT** 4  
**ENTRY** JN0471 #type complete  
**TITLE** protein-tyrosine kinase (EC 2.7.1.112) emb - mouse  
**ORGANISM** #formal\_name *Mus musculus* #common\_name house mouse  
**DATE** 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change  
 12-May-1995  
**ACCESSIONS** JN0471  
**REFERENCE** JN0471  
 #authors Yamada, N.; Kawakami, Y.; Kimura, H.; Fukamachi, H.; Baier,  
 G.; Altman, A.; Kato, T.; Inagaki, Y.; Kawakami, T.  
 #journal Biochem. Biophys. Res. Commun. (1993) 192:231-240  
 #title Structure and expression of novel protein-tyrosine kinases,  
 Emb and Eat, in the hematopoietic cells.  
 #accession JN0471  
 ##molecule\_type mRNA  
 ##residues 1-660 ##label YAM  
 ##note the nucleotide sequence is not given  
**GENETICS**  
 #gene emb  
**CLASSIFICATION** #superfamily SH3 homology; protein kinase homology; SH2  
 homology  
**KEYWORDS** phosphotransferase  
**FEATURE**  
 223-271 #domain SH3 homology ##label SH3\  
 283-379 #domain SH2 homology ##label SH2\  
 402-659 #domain protein kinase homology ##label KIN\  
 552 #binding\_site phosphate (Tyr) (covalent) #status  
 predicted  
**SUMMARY** #length 660 #molecular-weight 76577 #checksum 1680

Query Match 56.0%; Score 324; DB 12; Length 660;  
Best Local Similarity 47.5%; Pred. No. 1.26e-38;  
Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 283 wyskhmtrsqaeqllkqegkeggfivrdsskagkytvsvfakstgepqqvirhyvcstp 342  
|:: ::::|::|::|::| |::|::|::|::| |::|::|::|::| | |::|::|::|:  
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMYTSLFSKAVNDKKGTVKHYHVHTNA 355

Db 343 qsqyylaekhlfstipelin 362  
|:: |::|::| |::|::|:  
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 5

ENTRY A45184 #type fragment

TITLE B cell progenitor kinase - human (fragment)

CONTAINS tyrosine kinase

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change  
19-Oct-1995

ACCESSIONS A45184

REFERENCE A45184

#authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.;  
Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.;  
Mohandas, T.; Guan, S.; Belmont, J.W.; Cooper, M.D.;  
Conley, M.E.; Witte, O.N.

#journal Cell (1993) 72:279-290

#title Deficient expression of a B cell cytoplasmic tyrosine kinase  
in human X-linked agammaglobulinemia.

#cross-references MUID:93145329

#accession A45184

##status preliminary; not compared with conceptual translation

##molecule\_type nucleic acid

##residues 1-442 ##label TSU

##cross-references NCBI:123835

##experimental\_source erythroleukemia cell line K562

##note sequence extracted from NCBI backbone

CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
homology

FEATURE

221-269 #domain SH3 homology #label SH3\  
281-377 #domain SH2 homology #label SH2\  
400-442 #domain protein kinase homology (fragment) #label KIN

SUMMARY #length 442 #checksum 2964

Query Match 55.1%; Score 319; DB 11; Length 442;  
Best Local Similarity 47.5%; Pred. No. 9.71e-38;  
Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhmtrsqaeqllkqegkeggfivrdsskaakytvsvfakstgdpgqvirhyvcstp 340  
|:: ::::|::|::|::| |::|::|::|::| |::|::|::|::| | |::|::|::|:  
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMYTSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqyylaekhlfstipelin 360  
|:: |::|::| |::|::|:  
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 6

ENTRY S33253 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change  
19-Oct-1995

ACCESSIONS S33253

REFERENCE S33253

CC transformation. Such compounds have value in the treatment of  
CC chronic, acute myelogenous or acute lymphocytic leukaemia.  
SQ Sequence 1336 AA;

Query Match 7.7%; Score 85; DB 15; Length 1336;  
Best Local Similarity 27.3%; Pred. No. 9.62e+00;  
Matches 12; Conservative 15; Mismatches 15; Indels 2; Gaps 2

Db 515 kvqindkddtseykhafeiilkdgnsvifsaaksaeeknnuuaal 558  
|| :: : | : || : | || : : : | : : ||  
Qu 65 KVNLEE-QTPVERGYPFQIVVYKDGLLYVYASN-EESRSQWLKAL 106

Search completed: Mon Feb 3 16:54:34 1997  
Job time : 30 secs.

\*\*\*\*\*  
MAPLE  
\*\*\*\*\*  
TM

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:52:39 1997; MasPar time 6.14 Seconds  
607.923 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
Description: (25-169) from US08426509.pep (1 of 5)  
Perfect Score: 1102  
Sequence: 1 NYKERLFLVLTKTNLSSYYEYD.....ANLHTAVNEEKHRVPTFPDR 143

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann10  
14:unrev

Statistics: Mean 41.009; Variance 85.671; scale 0.479

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

22

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred	Na
--------	-------	-----	-------	-------	--------	----	----	-------------	------	----

1	447	40.6	602	4	JU0215	tyrosine kinase, tec	6.81e-62
2	447	40.6	608	4	JU0227	protein-tyrosine kin	6.81e-62
3	447	40.6	630	4	JU0228	protein tyrosine kin	6.81e-62
4	423	38.4	620	4	S33253	protein-tyrosine kin	2.39e-57
5	413	37.5	619	4	JN0472	protein-tyrosine kin	1.84e-55
6	413	37.5	619	4	A47333	T-cell-specific tyro	1.84e-55
7	368	33.4	625	4	A43030	protein-tyrosine kin	4.92e-47
8	314	28.5	442	11	A45184	B cell progenitor ki	4.39e-37
9	314	28.5	659	11	S28912	protein-tyrosine kin	4.39e-37
10	314	28.5	659	11	I37212	Bruton agammaglobuli	4.39e-37
11	314	28.5	660	12	JN0471	protein-tyrosine kin	4.39e-37
12	313	28.4	659	12	B45184	B cell progenitor ki	6.68e-37
13	225	20.4	847	12	A56039	GTPase-activating pr	2.97e-21
14	202	18.3	527	4	S13763	protein-tyrosine kin	2.46e-17
15	142	12.9	1165	11	A42142	gap1 protein - fruit	1.14e-07
16	142	12.9	1165	10	S27809	GTPase-activating pr	1.14e-07
17	116	10.5	205	7	JU0223	hypothetical 24K pro	7.29e-04
18	98	8.9	350	11	S00755	pleckstrin - human	1.90e-01
19	97	8.8	1042	4	A33881	Ca2+-transporting AT	2.55e-01
20	97	8.8	1042	1	PWRBMC	Ca2+-transporting AT	2.55e-01
21	92	8.3	218	9	S47016	hypothetical protein	1.08e+00
22	91	8.3	348	4	JN0633	caricain (EC 3.4.22.	1.43e+00
23	91	8.3	454	7	B64107	chromosomal replicat	1.43e+00
24	90	8.2	345	1	PPPA	papain (EC 3.4.22.2)	1.89e+00
25	90	8.2	2223	11	A47447	calcium channel prot	1.89e+00
26	88	8.0	549	9	S46029	hypothetical protein	3.29e+00
27	88	8.0	1928	12	JS0610	beta-galactosidase (	3.29e+00
28	87	7.9	328	9	S45998	hypothetical protein	4.33e+00
29	86	7.8	458	10	S57605	hypothetical protein	5.68e+00
30	86	7.8	704	14	S61612	hypothetical protein	5.68e+00
31	86	7.8	775	9	S35543	DNA-directed DNA pol	5.68e+00
32	86	7.8	1549	2	A40691	trichohyalin - sheep	5.68e+00
33	85	7.7	97	7	B37141	parC protein - Esche	7.43e+00
34	85	7.7	104	7	B47062	pyocin positive regu	7.43e+00
35	85	7.7	362	12	A38135	ADP-ribosylarginine	7.43e+00
36	85	7.7	807	11	A34581	oxysterol-binding pr	7.43e+00
37	85	7.7	809	12	A34404	oxysterol-binding pr	7.43e+00
38	85	7.7	1336	12	S25716	SDS-1 protein - mous	7.43e+00
39	85	7.7	1487	4	S15904	alpha-1 proteinase i	7.43e+00
40	84	7.6	329	8	H64143	hypothetical protein	9.71e+00
41	83	7.5	305	8	S47261	cheR protein - Rhodo	1.26e+01
42	83	7.5	2009	10	A31068	SEC7 protein - yeast	1.26e+01
43	82	7.4	813	11	B47485	ABR protein 2 - huma	1.64e+01
44	82	7.4	822	11	A47485	ABR protein 1 - huma	1.64e+01
45	82	7.4	1477	4	A29952	alpha-1-inhibitor II	1.64e+01

## ALIGNMENTS

RESULT 1  
 ENTRY JU0215 #type complete  
 TITLE tyrosine kinase, tec type II - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change  
 01-Dec-1995

ACCESSIONS JU0215  
 REFERENCE JU0215  
 #authors Mano, H.; Mano, K.; Copeland, N.; Ihle, J.N.  
 #submission submitted to JIPID, December 1991  
 #accession JU0215  
 ##molecule\_type mRNA  
 ##residues 1-602 ##label MAN  
 ##experimental\_source liver, strain Balb/c

## GENETICS

#gene ter

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
KEYWORDS kinase-related transforming protein  
FEATURE  
185-223 #domain SH3 homology #status atypical #label SH3  
345-602 #domain protein kinase homology #label KIN  
353-361 #region protein kinase ATP-binding motif  
496 #binding\_site phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
SUMMARY #length 602 #molecular-weight 70103 #checksum 7992

Query Match 40.6%; Score 447; DB 4; Length 602;  
Best Local Similarity 45.8%; Pred. No. 6.81e-62;  
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkvidiskikcveivknndgvipcqnkfpfqvv 83  
|||||| || |: ||||| : : |||| |: |||:||| |: :: | : :|||:  
Gy 25 NYKERLFVLTKTNLSYYEYDKMKRGSRKGSIEIKKIRCVKVNLEEQT-PVERQYPFQIV 83  
Db 84 hdantlyifapspqsrdruvkkkkeeeiknnnnniikyhpkfadgsyqccrqteklapgc 143  
||:||:||:|| |:|| | ||: | ::::|||: | || : ||:|: | |||||  
Gy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQGSCKAAPGC 143

RESULT 2  
ENTRY JU0227 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) tec III - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 01-Dec-1995  
ACCESSIONS JU0227  
REFERENCE JU0227  
#authors Mano, H.; Sato, K.; Yazaki, Y.; Hirai, H.  
#submission submitted to JIPID, March 1993  
#description The Tec protein-tyrosine kinase is involved in the IL-3 signaling pathway in a murine myeloid cell line.  
#accession JU0227  
##molecule\_type mRNA  
##residues 1-608 #label MAN  
GENETICS  
#gene Tec  
CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
KEYWORDS kinase-related transforming protein; phosphotransferase  
FEATURE  
185-223 #domain SH3 homology #status atypical #label SH3  
345-603 #domain protein kinase homology #label KIN  
496 #binding\_site phosphate (Tyr) (covalent) #status predicted  
SUMMARY #length 608 #molecular-weight 71162 #checksum 1974

Query Match 40.6%; Score 447; DB 4; Length 608;  
Best Local Similarity 45.8%; Pred. No. 6.81e-62;  
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkvidiskikcveivknndgvipcqnkfpfqvv 83  
|||||| || |: ||||| : : |||| |: |||:||| |: :: | : :|||:  
Gy 25 NYKERLFVLTKTNLSYYEYDKMKRGSRKGSIEIKKIRCVKVNLEEQT-PVERQYPFQIV 83  
Db 84 hdantlyifapspqsrdruvkkkkeeeiknnnnniikyhpkfadgsyqccrqteklapgc 143  
||:||:||:|| |:|| | ||: | ::::|||: | || : ||:|: | |||||  
Gy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQGSCKAAPGC 143

RESULT 3  
ENTRY JU0228 #type complete

**TITLE** protein tyrosine kinase (EC 2.7.1.-) tec IV - mouse  
**ORGANISM** #formal\_name *Mus musculus* #common\_name house mouse  
**DATE** 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
21-Mar-1996  
**ACCESSIONS** JU0228  
**REFERENCE** JU0228  
#authors Mano, H.; Sato, K.; Yazaki, Y.; Hirai, H.  
#submission submitted to JIPID, April 1993  
#accession JU0228  
##molecule\_type DNA  
##residues 1-630 ##label MAN  
##experimental\_source myeloid  
**CLASSIFICATION** #superfamily protein-tyrosine kinase src; protein kinase  
homology; SH2 homology; SH3 homology  
**KEYWORDS** kinase-related transforming protein; phosphotransferase  
**FEATURE**  
185-233 #domain SH3 homology #label SH3\  
246-344 #domain SH2 homology #label SH2\  
367-625 #domain protein kinase homology #label KIN\  
375-383 #region protein kinase ATP-binding motif\  
515 #active\_site Asp (aspartylphosphate intermediate)  
##status predicted  
**SUMMARY** #length 630 #molecular-weight 73651 #checksum 4354

Query Match 40.6%; Score 447; DB 4; Length 630;  
Best Local Similarity 45.8%; Pred. No. 6.81e-62;  
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2

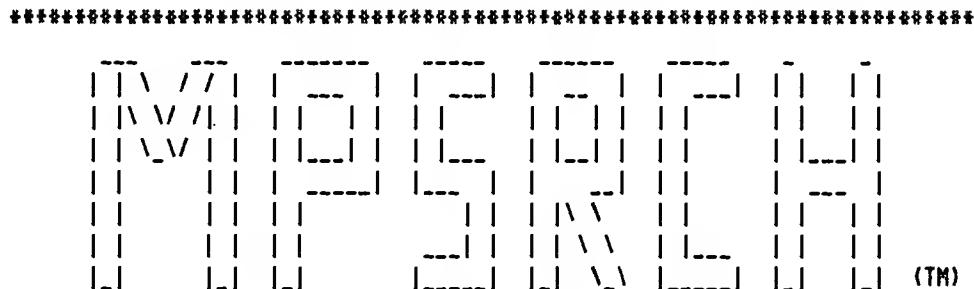
Db	25	nykerlcvlpksvlsyee-graekkyrkvgidiskikcveivknddgvipcqnkfpfqvv	83
		:         : :      :     :     :    :   :      :	
Qy	25	NYKERLFVLTKTNLSYYEYDKMKRGSRKGSIEIKKIRCKVEKVNLLEEQT-PVERGYPFQIV	83
Db	84	hdantlyifapspqsrdravkkllkeei knnnnnimikyhpkf wadgsyqccrqtek lapg c	14
		:   :   :   :        :  :   :   :   :   :   :   :        :   :	
Qy	84	YKDGLLYVYASNEEERSQWLKALQKEIRGNPHLLVKYHSGFFVUDGKFLCCQQSCKAAPGC	14

RESULT 4  
 ENTRY S33253 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change  
       19-Oct-1995  
 ACCESSIONS S33253  
 REFERENCE S33253  
   #authors Tanaka, N.; Asao, H.; Ohtani, K.; Nakanura, M.; Sugamura, K.  
   #journal FEBS Lett. (1993) 324:1-5  
   #title A novel human tyrosine kinase gene inducible in T cells by  
         interleukin 2.  
   #accession S33253  
   #status preliminary  
   ##molecule\_type mRNA  
   ##residues 1-620 ##label TAN  
   ##cross-references EMBL:D13720  
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology  
 KEYWORDS phosphotransferase  
 FEATURE  
   178-226       #domain SH3 homology #label SH3\  
   361-619       #domain protein kinase homology #label KIN  
 SUMMARY #length 620 #molecular-weight 71830 #checksum 8123

Query Match 38.4%; Score 423; DB 4; Length 620;  
Best Local Similarity 46.0%; Pred. No. 2.39e-57;  
Matches 57; Conservative 26; Mismatches 41; Indels 0; Gaps 0

Db 25 nfkvrffvltkaslaufedrhqkkr1lkasielksrikcveivksdisipchukupfqvh 8

Job time : 9 secs.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:02:47 1997; MasPar time 2.55 Seconds  
151.211 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-2  
Description: (493-507) from US08426509.pep (4 of 4)  
Perfect Score: 92  
Sequence: 1 GQDADGSTSPRSQEP 15

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 22.865; Variance 34.220; scale 0.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	% No. Score Match Length DB ID Description Pred. No.							
		No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	92	100.0	507	4	A55625			protein-tyrosine kin	4.02e-08
2	75	81.5	465	4	B55625			protein-tyrosine kin	1.99e-04
3	75	81.5	465	12	I48926			protein-tyrosine kin	1.99e-04
4	54	58.7	156	3	Q0BEG9			HHRF1 protein - huma	2.65e+00
5	54	58.7	755	12	S32103			filensin - bovine	2.65e+00
6	52	56.5	717	6	S31034			retrovirus-related g	6.01e+00
7	52	56.5	717	6	S31035			retrovirus-related g	6.01e+00
8	51	55.4	1004	9	JC2221			major surface glycop	8.99e+00
9	50	54.3	41	11	A47602			complement C3b/C4b r	1.34e+01
10	50	54.3	195	11	S31861			myristylated alanine	1.34e+01
11	50	54.3	200	12	S17185			myristoylated alanin	1.34e+01
12	50	54.3	226	12	A26964			neuronal growth-rela	1.34e+01
13	50	54.3	227	12	A29800			neuromodulin - mouse	1.34e+01

14	50	54.3	545	7	F64181	CTP synthetase (pyrG	1.34e+01
15	50	54.3	2039	11	S03843	complement C3b/C4b r	1.34e+01
16	49	53.3	133	5	S24315	motilin precursor -	1.98e+01
17	49	53.3	351	12	A56387	helix-loop-helix tra	1.98e+01
18	49	53.3	436	7	S13583	nosD protein precurs	1.98e+01
19	49	53.3	471	7	S35635	DNA injection protei	1.98e+01
20	49	53.3	590	12	A40437	glutamic acid-rich p	1.98e+01
21	49	53.3	926	12	A54142	nucleoporin NUP107 -	1.98e+01
22	48	52.2	188	10	S44817	F44E2.2 protein - Ca	2.92e+01
23	48	52.2	559	11	B56731	chromatin assembly f	2.92e+01
24	48	52.2	627	10	A44112	spidroin 2, dragline	2.92e+01
25	48	52.2	1101	8	S15271	endoglucanase cenC -	2.92e+01
26	48	52.2	1396	12	A44453	translation initiati	2.92e+01
27	48	52.2	3566	11	A40701	tenascin-X precursor	2.92e+01
28	47	51.1	179	12	JH0499	glutamine/glutamic a	4.28e+01
29	47	51.1	189	14	D49600	genome-linked protei	4.28e+01
30	47	51.1	190	2	RHSHCE	corticoliberin precu	4.28e+01
31	47	51.1	315	6	D48560	immediate-early prot	4.28e+01
32	47	51.1	332	10	S60935	Lpe17 protein - yeas	4.28e+01
33	47	51.1	357	6	S18236	omega secalin precur	4.28e+01
34	47	51.1	357	6	S18235	omega secalin precur	4.28e+01
35	47	51.1	401	14	S58355	CP49 protein - chick	4.28e+01
36	47	51.1	425	5	A26431	nerve growth factor	4.28e+01
37	47	51.1	427	2	G0HUN	nerve growth factor	4.28e+01
38	47	51.1	450	11	S58351	CP49ins protein - ch	4.28e+01
39	47	51.1	479	11	A34924	complement C3b/C4b r	4.28e+01
40	47	51.1	591	11	A45135	profilaggrin - human	4.28e+01
41	47	51.1	664	2	VEHULA	lamin A - human	4.28e+01
42	47	51.1	713	11	S42803	fibroblast growth fa	4.28e+01
43	47	51.1	775	3	EDBE11	immediate-early prot	4.28e+01
44	47	51.1	1772	10	A45532	major merozoite surf	4.28e+01
45	47	51.1	2248	11	A35938	profilaggrin - human	4.28e+01

## ALIGNMENTS

RESULT	1
ENTRY	A55625 #type complete
TITLE	protein-tyrosine kinase (EC 2.7.1.112), megakaryocyte-associated - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 01-Mar-1996
ACCESSIONS	A55625; S43533
REFERENCE	A55625
#authors	Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham, H.
#journal	J. Biol. Chem. (1995) 270:1833-1842
#title	Structural and functional studies of the intracellular tyrosine kinase MATK gene and its translated product.
#accession	A55625
	##status preliminary; not compared with conceptual translation
	##molecule_type DNA
	##residues 1-507 ##label AVR
REFERENCE	S43533
#authors	Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.; Suda, T.
#journal	Oncogene (1994) 9:1155-1161
#title	Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic consensus tyrosine-lacking kinase).
#accession	S43533
	##status preliminary
	##molecule_type mRNA
	##residues 1-507 ##label SAK
	##cross-references EMBL:X77278

**gene** GDB:MATK  
**##cross-references** GDB:GOO-304-667  
**CLASSIFICATION** #superfamily SH2 homology; protein kinase homology; SH3 homology  
**KEYWORDS** phosphotransferase  
**FEATURE**  
 55-105 #domain SH3 homology #label SH31\  
 122-211 #domain SH2 homology #label SH2\  
 233-485 #domain protein kinase homology #label KIN  
**SUMMARY** #length 507 #molecular-weight 56469 #checksum 6051

Query Match 100.0%; Score 92; DB 4; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 4.02e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 493 gqdadgstsprsqep 507  
 |||||||  
 Qy 493 GQDADGSTSPRSQEP 507

**RESULT** 2  
**ENTRY** B55625 #type complete  
**TITLE** protein-tyrosine kinase (EC 2.7.1.112),  
 megakaryocyte-associated - mouse  
**ORGANISM** #formal\_name Mus musculus #common\_name house mouse  
**DATE** 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change  
 19-Oct-1995  
**ACCESSIONS** B55625  
**REFERENCE** A55625  
 #authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,  
 L.L.; White, R.A.; Avraham, H.  
 #journal J. Biol. Chem. (1995) 270:1833-1842  
 #title Structural and functional studies of the intracellular  
 tyrosine kinase MATK gene and its translated product.  
 #accession B55625  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type mRNA  
 ##residues 1-465 #label AVR  
**CLASSIFICATION** #superfamily SH3 homology; protein kinase homology; SH2 homology  
**KEYWORDS** phosphotransferase  
**FEATURE**  
 13-63 #domain SH3 homology #label SH31\  
 80-169 #domain SH2 homology #label SH2\  
 191-443 #domain protein kinase homology #label KIN  
**SUMMARY** #length 465 #molecular-weight 51585 #checksum 6919

Query Match 81.5%; Score 75; DB 4; Length 465;  
 Best Local Similarity 60.0%; Pred. No. 1.99e-04;  
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 451 gqeaegeapsaptrsqdq 465  
 ||:||:||:||:||:  
 Qy 493 GQDADGSTSPRSQEP 507

**RESULT** 3  
**ENTRY** I48926 #type complete  
**TITLE** protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse  
**ALTERNATE\_NAMES** csk-type protein-tyrosine kinase  
**ORGANISM** #formal\_name Mus musculus #common\_name house mouse  
**DATE** 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change  
 15-Mar-1996  
**ACCESSIONS** I48926  
**REFERENCE** A53469  
 #authors Klages, S.; Adam, D.; Class, K.; Faronoli, J.; Bolen, J.B.;

CC to SH2 regions of Src, Abl, Lck and p85-alpha-N (R72088-91,

CC respectively).  
CA Sequence 99 AA:

Query Match 31.7%; Score 187; DB 13; Length 99;  
Best Local Similarity 32.9%; Pred. No. 1.98e-09;  
Matches 25; Conservative 23; Mismatches 27; Indels 1; Gaps 1

Db 5 wywgdisreevnekrlrdtagtflyrdastknhgdyltlrkggnnklikifhrdgkygf 64

Qy 122 WFHGKISGQEAVQQLQPPEDGLFLVRE-SARHPGDYVLCSVFGRDVIGHYRVLHRDGHLTI 180

Db 65 sdpltfnsvvvelinhy 80  
.....

181 DEAUVILLE MURPHY 186

Search completed: Mon Feb 3 17:02:02 1997

Job time is 6 secs.

11. *Leucosia* *leucostoma* (Fabricius) (Fabricius, 1775: 400). Type locality: “India, Madras, Madrasa, 1773”.

MAP

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:01:07 1997; MasPar time 4.29 Seconds  
450,074 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-2  
Description: (122-196) from US08426509.pep (3 of 4)  
Perfect Score: 590  
Sequence: 1 WEHGKISCREAVQQLQPPED... HLTIDEA

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

## Post-processing: Minimum Match 0%

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann10  
14:unann11

Statistics: Mean 38.199; Variance 81.461; scale 0.469

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query					Description	Pred. No.
	No.	Score	Match	Length	DB ID		
1	590	100.0	507	4	A55625	protein-tyrosine kin	4.42e-89
2	590	100.0	527	11	A49865	protein-tyrosine kin	4.42e-89
3	570	96.6	465	4	B55625	protein-tyrosine kin	2.92e-85
4	570	96.6	465	12	I48926	protein-tyrosine kin	2.92e-85
5	350	59.3	450	1	JH0559	protein-tyrosine kin	5.07e-44
6	349	59.2	450	12	I48929	protein-tyrosine kin	7.73e-44
7	349	59.2	450	1	S15094	protein-tyrosine kin	7.73e-44
8	344	58.3	450	4	A41973	protein-tyrosine kin	6.33e-43
9	215	36.4	723	12	B38749	3-phosphatidylinosit	4.48e-20
10	202	34.2	451	12	S49016	tyrosine kinase - hu	7.01e-18
11	199	33.7	217	12	A54688	modular adaptor Grb2	2.23e-17
12	199	33.7	217	11	A43321	growth factor recept	2.23e-17
13	199	33.7	217	12	S26050	gene ash protein - r	2.23e-17
14	195	33.1	841	11	A43254	protein-tyrosine-pho	1.04e-16
15	194	32.9	217	11	JT0664	growth factor recept	1.52e-16
16	192	32.5	724	11	A38748	3-phosphatidylinosit	3.27e-16
17	191	32.4	239	12	A46243	epidermal growth fac	4.79e-16
18	191	32.4	612	11	JC2197	protein-tyrosine kin	4.79e-16
19	191	32.4	635	11	JC2198	protein-tyrosine kin	4.79e-16
20	191	32.4	635	11	A53596	protein-tyrosine kin	4.79e-16
21	187	31.7	628	12	S57436	protein-tyrosine kin	2.19e-15
22	187	31.7	724	12	A38747	phosphatidylinositol	2.19e-15
23	187	31.7	724	12	A38749	3-phosphatidylinosit	2.19e-15
24	185	31.4	204	5	B45022	CRK-I - human	4.68e-15
25	185	31.4	304	5	A45022	CRK-II - human	4.68e-15
26	180	30.5	303	5	S41754	CRKL protein - human	3.09e-14
27	180	30.5	605	12	B56707	protein-tyrosine kin	3.09e-14
28	180	30.5	628	12	A56707	protein-tyrosine kin	3.09e-14
29	178	30.2	303	12	S58352	SH2/SH3 adaptor prot	6.56e-14
30	178	30.2	557	10	A00629	protein-tyrosine kin	6.56e-14
31	174	29.5	209	11	A48090	alpha 2-chimerin, p4	2.93e-13
32	173	29.3	870	11	B40121	GTPase-activating pr	4.26e-13
33	173	29.3	1047	11	A40121	GTPase-activating pr	4.26e-13
34	172	29.2	1038	12	JT0663	ras GTPase-activatin	6.18e-13
35	172	29.2	1044	12	S01966	GTPase-activating pr	6.18e-13
36	171	29.0	535	12	C46243	epidermal growth fac	8.96e-13
37	169	28.6	505	4	S24550	protein-tyrosine kin	1.88e-12
38	166	28.1	443	12	B53764	beta2-chimaerin, cer	5.70e-12
39	166	28.1	466	11	A53764	beta2-chimaerin, cer	5.70e-12
40	166	28.1	628	12	A40802	protein-tyrosine kin	5.70e-12
41	164	27.8	1236	10	A53970	1-phosphatidylinosit	1.19e-11
42	162	27.5	232	2	TVFV10	transforming protein	2.48e-11
43	162	27.5	305	5	A49011	c-Crk - chicken	2.48e-11
44	161	27.3	211	10	A46444	SH2-SH3 adaptor prot	3.57e-11
45	161	27.3	595	4	A55651	protein-tyrosine-pho	3.57e-11

## ALIGNMENTS

RESULT	1
ENTRY	A55625 #type complete
TITLE	protein-tyrosine kinase (EC 2.7.1.112), megakaryocyte-associated - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 01-Mar-1996
ACCESSIONS	A55625; S43533
REFERENCE	A55625
#authors	Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham, H.
#journal	J. Biol. Chem. (1995) 270:1833-1842

#title Structural and functional studies of the intracellular tyrosine kinase MATK gene and its translated product.  
#accession A55625  
##status preliminary; not compared with conceptual translation  
##molecule\_type DNA  
##residues 1-507 ##label AVR  
REFERENCE S43533  
#authors Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.; Suda, T.  
#journal Oncogene (1994) 9:1155-1161  
#title Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic consensus tyrosine-lacking kinase).  
#accession S43533  
##status preliminary  
##molecule\_type mRNA  
##residues 1-507 ##label SAK  
##cross-references EMBL:X77278

## GENETICS

#gene GDB:MATK  
##cross-references GDB:G00-304-667

CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3 homology

KEYWORDS phosphotransferase

## FEATURE

55-105 #domain SH3 homology ##label SH3I  
122-211 #domain SH2 homology ##label SH2I  
233-485 #domain protein kinase homology ##label KIN

SUMMARY #length 507 #molecular-weight 56469 #checksum 6051

Query Match 100.0%; Score 590; DB 4; Length 507;  
Best Local Similarity 100.0%; Pred. No. 4.42e-89;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 wfhgkisgqeavqqlqpppedglflvresarhpgdyvlcvsgfrdvihyrvlhrgdghltid 181  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 122 WFGKISGQEAVQQLQPPPEDGLFLVRESARHPGDYVLCVSGFRDVIHYRVLHRDGHLID 181

Db 182 eavffcnlmdmvehy 196  
|||||||||||||||

Qy 182 EAVFFCNLMDMVEHY 196

## RESULT 2

ENTRY A49865 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) matk - human  
ALTERNATE\_NAMES megakaryocyte-associated tyrosine kinase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 30-Jun-1995 #sequence\_revision 30-Jun-1995 #text\_change  
19-Oct-1995  
ACCESSIONS A49865  
REFERENCE A49865  
#authors Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.; Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.  
#journal J. Biol. Chem. (1994) 269:1068-1074  
#title Identification and characterization of a novel tyrosine kinase from megakaryocytes.  
#accession A49865  
##status preliminary  
##molecule\_type mRNA  
##residues 1-527 ##label BEN  
##cross-references GB:L18974  
CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3 homology  
KEYWORDS phosphotransferase  
FEATURE  
55-105 #domain SH3 homology ##label SH3I

122-211                    #domain SH2 homology #label SH2\\  
233-484                    #domain protein kinase homology #label KIN  
SUMMARY                    #length 527 #molecular-weight 58473 #checksum 1630

Query Match                100.0%; Score 590; DB 11; Length 527;  
Best Local Similarity 100.0%; Pred. No. 4.42e-89;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 wfhgkisgqeavqqlpqppedglflvresarhpgdyvlcvsgfrdvihyrvlhrgdghltid 181  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 122 WFGKISGQEAVQQLPQPPEDGLFLVRESARHPGDYVLCVSGFRDVIHYRVLHRDGHLTID 181

Db 182 eavffcnlmdmvehy 196  
|||||||||||||||

Qy 182 EAVFFCNLMDMVEHY 196

RESULT 3

ENTRY                    B55625 #type complete  
TITLE                    protein-tyrosine kinase (EC 2.7.1.112),  
                          megakaryocyte-associated - mouse  
ORGANISM                #formal\_name Mus musculus #common\_name house mouse  
DATE                    24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change  
                          19-Oct-1995  
ACCESSIONS              B55625  
REFERENCE               A55625  
#authors                Abraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,  
                          L.L.; White, R.A.; Abraham, H.  
#journal               J. Biol. Chem. (1995) 270:1833-1842  
#title                 Structural and functional studies of the intracellular  
                          tyrosine kinase MATK gene and its translated product.  
#accession              B55625  
##status                preliminary; not compared with conceptual translation  
##molecule\_type        mRNA  
##residues             1-465 #label AVR  
CLASSIFICATION        #superfamily SH3 homology; protein kinase homology; SH2  
                          homology  
KEYWORDS                phosphotransferase  
FEATURE  
13-63                    #domain SH3 homology #label SH3\\  
80-169                    #domain SH2 homology #label SH2\\  
191-443                 #domain protein kinase homology #label KIN  
SUMMARY                 #length 465 #molecular-weight 51585 #checksum 6919

Query Match                96.6%; Score 570; DB 4; Length 465;  
Best Local Similarity 97.3%; Pred. No. 2.92e-85;  
Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 wfhgkisgqeaiqqlpqppedglflvresarhpgdyvlcvsgfrdvihyrvlhrgdghltid 139  
|||||||||:||||||||||||||||||||||||||||||||||||||||||||

Qy 122 WFGKISGQEAVQQLPQPPEDGLFLVRESARHPGDYVLCVSGFRDVIHYRVLHRDGHLTID 181

Db 140 eavcfcnlmdmvehy 154  
||| |||||||||

Qy 182 EAVFFCNLMDMVEHY 196

RESULT 4

ENTRY                    I48926 #type complete  
TITLE                    protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse  
ALTERNATE\_NAMES        csk-type protein-tyrosine kinase  
ORGANISM               #formal\_name Mus musculus #common\_name house mouse  
DATE                    15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change  
                          15-Mar-1996  
ACCESSIONS              I48926  
REFERENCE               A53469

#authors Klages, S.; Adam, D.; Class, K.; Farnnoli, J.; Bolen, J.B.;  
 Penhallow, R.C.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601  
 #title Ctk: a protein-tyrosine kinase related to Csk that defines an  
 enzyme family.  
 #cross-references MUID:94195789  
 #accession I48926  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-465 ##label RES  
 ##cross-references EMBL:U05210; NID:g450232; CDS\_PID:g450233  
 KEYWORDS phosphotransferase  
 SUMMARY #length 465 #molecular-weight 51495 #checksum 6748

Query Match 96.6%; Score 570; DB 12; Length 465;  
 Best Local Similarity 97.3%; Pred. No. 2.92e-85;  
 Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 wfhgkisgqeaiqqlqpppedglflvresarhpgdyvlcvsfgrdviyrvlhrdghltid 139  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Gy 122 WFGKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHLTID 181  
 Db 140 eavfcfnlmdmvehy 154  
 |||:|||||:  
 Gy 182 EAVFFCNLMDMVEHY 196

RESULT 5  
 ENTRY JH0559 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) CSK - human  
 ALTERNATE\_NAMES protein-tyrosine kinase cyl; protein-tyrosine kinase T2  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 30-Jun-1992 #sequence\_revision 20-Aug-1994 #text\_change  
 16-Feb-1996  
 ACCESSIONS JH0559; S38818; S19024; S19025  
 REFERENCE JH0559  
 #authors Braeuninger, A.; Holtrich, U.; Strebhardt, K.;  
 Ruebsamen-Waigmann, H.  
 #journal Gene (1992) 110:205-211  
 #title Isolation and characterization of a human gene that encodes a  
 new subclass of protein tyrosine kinases.  
 #cross-references MUID:92165060  
 #accession JH0559  
 ##molecule\_type mRNA  
 ##residues 1-450 ##label BRA  
 ##cross-references EMBL:X59932  
 ##experimental\_source lung  
 REFERENCE S38818  
 #authors Braeuninger, A.; Karn, T.; Strebhardt, K.;  
 Ruebsamen-Waigmann, H.  
 #journal Oncogene (1993) 8:1365-1369  
 #title Characterization of the human CSK locus.  
 #accession S38818  
 ##status preliminary  
 ##molecule\_type DNA  
 ##residues 1-450 ##label BR2  
 ##cross-references EMBL:X74765  
 REFERENCE S19024  
 #authors Partanen, J.; Armstrong, E.; Bergman, M.; Maekelae, T.P.;  
 Hirvonen, H.; Huebner, K.; Alitalo, K.  
 #journal Oncogene (1991) 6:2013-2018  
 #title cyl encodes a putative cytoplasmic tyrosine kinase lacking  
 the conserved tyrosine autophosphorylation site (Y416  
 (src)).  
 #cross-references MUID:92050797  
 #accession S19024

Run on: Mon Feb 3 17:11:18 1997; MasPar time 9.20 Seconds  
671.122 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-6  
Description: (247-486) from US08426509.pep (3 of 3)  
Perfect Score: 1791  
Sequence: I GSGQFGEVWEGLWNNTTPVA.....QFYNIMLECWNAEPKERPTF 240

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:anni 2:ann2 3:ann3 4:unanni 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 45.069; Variance 114.513; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	%	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1775	99.1	505	11	I38396				protein-tyrosine kin	8.20e-266
2	1272	71.0	505	4	S24550				protein-tyrosine kin	2.96e-182
3	1268	70.8	506	4	S24553				protein-tyrosine kin	1.35e-181
4	1203	67.2	362	4	S24551				protein-tyrosine kin	7.25e-171
5	1189	66.4	334	4	S24552				protein-tyrosine kin	1.47e-168
6	1114	62.2	509	1	TVHAST				protein-tyrosine kin	3.27e-156
7	1089	60.8	507	4	A39939				protein-tyrosine kin	4.20e-152
8	1074	60.0	536	4	S33569				protein-tyrosine kin	1.22e-149
9	1070	59.7	512	4	A39719				protein-tyrosine kin	5.54e-149
10	1070	59.7	512	1	TVHULY				protein-tyrosine kin	5.54e-149
11	1063	59.4	539	11	B49114				protein-tyrosine kin	7.81e-148
12	1060	59.2	542	11	A49114				protein-tyrosine kin	2.43e-147
13	1056	59.0	532	4	A34104				protein-tyrosine kin	1.10e-146
14	1056	59.0	532	4	B34104				protein-tyrosine kin	1.10e-146
15	1051	58.7	505	1	TVHUHC				protein-tyrosine kin	7.27e-146
16	1051	58.7	542	1	TVHUSC				protein-tyrosine kin	7.27e-146
17	1049	58.6	541	4	A43610				protein-tyrosine kin	1.55e-145
18	1045	58.3	526	4	S15582				protein-tyrosine kin	7.00e-145
19	1044	58.3	557	1	TVFV52				protein-tyrosine kin	1.02e-144
20	1044	58.3	587	1	TVFVPR				protein-tyrosine kin	1.02e-144
21	1043	58.2	526	1	TVFV60				protein-tyrosine kin	1.49e-144
22	1042	58.2	526	1	TVFVR				protein-tyrosine kin	2.17e-144
23	1043	58.2	533	1	TVCHS				protein-tyrosine kin	1.49e-144
24	1040	58.1	503	1	TVMSHC				protein-tyrosine kin	4.63e-144
25	1040	58.1	537	4	A43806				protein-tyrosine kin	4.63e-144
26	1039	58.0	526	4	S20808				protein-tyrosine kin	6.75e-144
27	1039	58.0	526	1	OKFVYR				protein-tyrosine kin	6.75e-144
28	1038	58.0	568	1	TVFV51				protein-tyrosine kin	9.84e-144
29	1037	57.9	509	4	A23639				protein-tyrosine kin	1.44e-143
30	1035	57.8	503	4	JQ1321				protein-tyrosine kin	3.05e-143
31	1036	57.8	537	1	TVHUSY				protein-tyrosine kin	2.09e-143
32	1034	57.7	392	4	S04205				protein-tyrosine kin	4.45e-143

33	1034	57.7	523	1	TVFVMT	protein-tyrosine kin	4.45e-143
34	1032	57.6	526	7	S20676	protein-tyrosine kin	9.47e-143
35	1032	57.6	526	7	S26420	src protein - Rous s	9.47e-143
36	1030	57.5	509	1	OKHULK	protein-tyrosine kin	2.02e-142
37	1029	57.5	537	1	TVHUSR	protein-tyrosine kin	2.94e-142
38	1026	57.3	663	1	TVMVRR	protein-tyrosine kin	9.12e-142
39	1024	57.2	529	1	TVHUFR	protein-tyrosine kin	1.94e-141
40	1022	57.1	517	12	S24547	protein-tyrosine kin	4.12e-141
41	1022	57.1	541	1	TVCHYS	protein-tyrosine kin	4.12e-141
42	1023	57.1	545	7	S52313	pp62v protein - Rous	2.83e-141
43	1022	57.1	546	7	S52314	pp62v protein - Rous	4.12e-141
44	1016	56.7	537	4	A45501	protein-tyrosine kin	3.96e-140
45	1016	56.7	541	12	S31645	protein-turosine kin	3.96e-140

## ALIGNMENTS

RESULT 1  
ENTRY I38396 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human  
ALTERNATE\_NAMES FYN-related kinase (FRK)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change  
15-Mar-1996  
ACCESSIONS I38396  
REFERENCE I38396  
#authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.  
#journal Gene (1994) 138:247-251  
#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.  
#cross-references MUID:94171047  
#accession I38396  
##status preliminary  
##molecule\_type mRNA  
##residues 1-505 ##label RES  
##cross-references EMBL:U00803; NID:g392887; CDS\_PID:g392888

GENETICS  
#gene GDB:FRK  
#cross-references GDB:G00-355-675  
KEYWORDS phosphotransferase  
SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 99.1%; Score 1775; DB 11; Length 505;  
Best Local Similarity 99.6%; Pred. No. 8.20e-266;  
Matches 239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 241 gsgqfgevweglwnnnttpavktlkpgsmdpndflreaqimknlrhpkliqlqavctled 300  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Au 247 CSCAECEVWECI WNNNTTPAUAKTI KPCSMDPNDFLREAQIMKNLRHPKLQLQAVCTLED 304

Db 301 p*g*iit*e*lmrhgslq*e*yl*q*ndtgskihltqqvdnaaqvasgmaylesrnyihrdlaarnv 360  
|||||||  
Ee 707 P*g*IXXIT*E*LMRHGSLQ*E*YL*Q*NDTGSKIHLTQQVDNAAQVASGMA  
|||||||  
744

Db 421 illyeiitygkmpysgmtgaqvigalaqnyrlpqpsncpqqfyinialecunaepkerptf 480  
|||||||  
Qy 427 ILLYEIIITYGKMPYSGMTGAQVIGMLAQNRYRLPQPSNCPQQFYINIMLECWNAEPKERPTF 486

RESULT 2  
ENTRY S24550 #type complete  
TITLE protein-tirosine kinase (EC 2.7.1.112) 1 - freshwater sponge

**ALTERNATE\_NAMES** (Spongilla lacustris)  
**ORGANISM** src-type tyrosine kinase 1  
**DATE** #formal\_name Spongilla lacustris  
07-May-1993 #sequence\_revision 07-May-1993 #text\_change  
03-Nov-1995  
**ACCESSIONS** S24550  
**REFERENCE** S24550  
#authors Raulf, F.  
#submission submitted to the EMBL Data Library, September 1991  
#accession S24550  
##molecule\_type mRNA  
##residues 1-505 ##label RAU  
##cross-references EMBL:X61601  
**GENETICS**  
#gene srk1  
**CLASSIFICATION** #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
**KEYWORDS** ATP; phosphotransferase; tyrosine-specific protein kinase  
**FEATURE**  
61-111 #domain SH3 homology ##label SH3\  
122-214 #domain SH2 homology ##label SH2\  
238-496 #domain protein kinase homology ##label KIN\  
246-254 #region protein kinase ATP-binding motif\  
268 #active\_site Lys ##status predicted  
**SUMMARY** #length 505 #molecular-weight 57693 #checksum 3389

Query Match 71.0%; Score 1272; DB 4; Length 505;  
Best Local Similarity 67.5%; Pred. No. 2.96e-182;  
Matches 162; Conservative 40; Mismatches 34; Indels 4; Gaps 3;

Db 247 gagqfgevweglwgnttsavktlkpgtmsveeflqeasimkrlrhpkliqlyavctkee 306  
||:|||||||||| ||:||||||| :|| :||:|| || ||:||||||| :||:  
Qy 247 GSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDLREAQIMKNLRHPKLIQLYAVCTLED 306

Db 307 piyivtelmkygsilleylrgedgv-lkieqlvdvaaqvasgnsyleqqnyihrdlaarni 365  
||||:||||: ||| |||: :| :| :| :||:|||||||:||| :|||||||:  
Qy 307 PIYIITELMRHGSLOEYLQNDTGSKIHLTQGYDMAAQVASGMAYLESRNYIHRDLAARNV 366

Db 366 lvgehgickvadfglarv--id-eeiyeahtgakfpikutapeaanynrftiksdyusfg 422  
||||| | ||||||||| :| :|||:| :||:||||||| :|:|||||||:  
Qy 367 LVGEHNIYKVADFGCLARVFVVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG 426

Db 423 vvlgeiitygrfpypgtnpevlekiqqnyrmpcpancpkqfhdiadcdwredpasrptf 482  
::|||||||: ||:||| :||:|||:|||:|||:|||:|||:|||:|||:  
Qy 427 ILLYEIITYGKMPYSGMTGAQVIQMLAGNYRLPQPSNCPQQFYNIMLECWNAEPKERPTF 486

**RESULT** 3  
**ENTRY** S24553 #type complete  
**TITLE** protein-tyrosine kinase (EC 2.7.1.112) 4 - freshwater sponge  
(Spongilla lacustris)  
**ALTERNATE\_NAMES** src-type tyrosine kinase 4  
**ORGANISM** #formal\_name Spongilla lacustris  
**DATE** 07-May-1993 #sequence\_revision 07-May-1993 #text\_change  
03-Nov-1995  
**ACCESSIONS** S24553  
**REFERENCE** S24550  
#authors Raulf, F.  
#submission submitted to the EMBL Data Library, September 1991  
#accession S24553  
##molecule\_type mRNA  
##residues 1-506 ##label RAU  
##cross-references EMBL:X61604  
**GENETICS**  
#gene srk4  
**CLASSIFICATION** #superfamily protein-tyrosine kinase src; protein kinase

KEYWORDS homology; SH2 homology; SH3 homology  
 FEATURE ATP; phosphotransferase; tyrosine-specific protein kinase  
 61-111 #domain SH3 homology #label SH3\  
 122-214 #domain SH2 homology #label SH2\  
 238-496 #domain protein kinase homology #label KIN\  
 246-254 #region protein kinase ATP-binding motif\  
 268 #active\_site Lys #status predicted  
 SUMMARY #length 506 #molecular-weight 57561 #checksum 9002

Query Match 70.8%; Score 1268; DB 4; Length 506;  
 Best Local Similarity 66.7%; Pred. No. 1.35e-181;  
 Matches 160; Conservative 40; Mismatches 36; Indels 4; Gaps 3;

Db 247 gagqfgevweglwnngttsavktlkpgtmsieefleasimkqlrhpkliqllyavctkee 306  
 |:|||||:||||| ||:|||||:|| ::|| || || |||||||:||||| :|:  
 Qy 247 GSGQFGEVWEGLWNNTTPAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED 306

Db 307 piyivtelmkhgsllsleylrgd-grsllklpdlvdacsqvasgnsyleqqnyihrdlaarni 365  
 ||||:||||:|||| ||||: || : || : || :||||:||| :|||||:||||:  
 Qy 307 PIYIITELMRHGSLOEYLNNDTGSKIHLTQQYDMAAQVASGMAYLESRNYIHRDLAARNV 366

Db 366 lvgehkickvadfglarv--id-eeiyeaklgakfpikwtapeaamysrftiksdvwsfg 422  
 |||||:| ||||||| :| :|||:| :||:||||| :||:|||||:  
 Qy 367 LVGEHNIYKVADFGGLARVFVVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG 426

Db 423 ivlyevitygrfpypgtnaqvleqiqqsyrmprpmgcpeklyaimmdcwredpasrptf 482  
 ||:|||:||||: ||:||| ||||: : ||:|||:||| ||: :| ||:|||:||| :| ||||:  
 Qy 427 ILLYEIITYGKMPYSGMTGAQVIVQMLAGNYRLPQPSNCPQQFYNIMLECWNAEPKERPTF 486

RESULT 4

ENTRY S24551 #type fragment  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 2 - freshwater sponge  
 (Spongilla lacustris) (fragment)  
 ALTERNATE\_NAMES src-type tyrosine kinase 2  
 ORGANISM #formal\_name Spongilla lacustris  
 DATE 07-May-1993 #sequence\_revision 07-May-1993 #text\_change  
 03-Nov-1995  
 ACCESSIONS S24551  
 REFERENCE S24550  
 #authors Raulf, F.  
 #submission submitted to the EMBL Data Library, September 1991  
 #accession S24551  
 ##molecule\_type mRNA  
 ##residues 1-362 ##label RAU  
 ##cross-references EMBL:X61602

GENETICS  
 #gene srk2

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
 homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE  
 1-70 #domain SH2 homology (fragment) #label SH2\  
 93-351 #domain protein kinase homology #label KIN\  
 101-109 #region protein kinase ATP-binding motif\  
 123 #active\_site Lys #status predicted  
 SUMMARY #length 362 #checksum 2776

Query Match 67.2%; Score 1203; DB 4; Length 362;  
 Best Local Similarity 64.6%; Pred. No. 7.25e-171;  
 Matches 155; Conservative 44; Mismatches 37; Indels 4; Gaps 4;

Db 102 gagqfgevyqglwnnstpvavktlkagtqpaaflaeaqimkklrhpkliqllyavctqge 161  
 |:||||| :|||||:|||||:|||:|| | |||||||:|||||:|||||:  
 Qy 247 GSGQFGEVWEGLWNNTTPAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED 306

Query Match 24.3%; Score 107; DB 9; Length 48;  
Best Local Similarity 53.6%; Pred. No. 4.51e-02;  
Matches 15; Conservative 7; Mismatches 4; Indels 2; Gaps 2

Db 6 alydyearteddsfekgek-fq-medl 31  
||:||:||:||:||:||:||:||:||:||:||:||  
Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDL 81

Search completed: Mon Feb 3 17:10:17 1997  
Job time : 9 secs.

\*\*\*\*\*  
MAPLE  
\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:09:24 1997; MasPar time 3.90 Seconds  
389.446 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-426-509-6  
Description: (54-112) from US08426509.pep (2 of 3)  
Perfect Score: 440  
Sequence: 1 ALFDYQARTAEDLSFRAGDKI.....KRRDGSSQQLQGYIIPSNYVA 59

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:anni 2:ann2 3:ann3 4:unanni 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unprey

Statistics: Mean 36.207; Variance 80.441; scale 0.450

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

21

Result	Query						Description	Pred. No.
	No.	Score	Match	Length	DB	ID		
1	422	95.9	505	11	I38396		protein-tyrosine kin	6.98e-56
2	191	43.4	509	1	TVHAST		protein-tyrosine kin	6.03e-16

3	170	38.6	532	4	B34104	protein-tyrosine kin	1.33e-12
4	167	38.0	542	11	A49114	protein-tyrosine kin	3.92e-12
5	166	37.7	534	4	A44991	protein-tyrosine kin	5.62e-12
6	166	37.7	534	4	S33568	protein-tyrosine kin	5.62e-12
7	166	37.7	537	1	TVHUSY	protein-tyrosine kin	5.62e-12
8	166	37.7	537	1	TVHUSR	protein-tyrosine kin	5.62e-12
9	166	37.7	537	4	A45501	protein-tyrosine kin	5.62e-12
10	165	37.5	532	4	A34104	protein-tyrosine kin	8.04e-12
11	165	37.5	537	4	A43806	protein-tyrosine kin	8.04e-12
12	165	37.5	543	1	TVHUY5	protein-tyrosine kin	8.04e-12
13	162	36.8	541	12	S31645	protein-tyrosine kin	2.36e-11
14	161	36.6	517	12	S24547	protein-tyrosine kin	3.37e-11
15	160	36.4	528	1	TVFVG9	protein-tyrosine kin	4.81e-11
16	160	36.4	529	1	TVHUF8	protein-tyrosine kin	4.81e-11
17	160	36.4	541	1	TVCHYS	protein-tyrosine kin	4.81e-11
18	158	35.9	533	1	TVCHS	protein-tyrosine kin	9.79e-11
19	158	35.9	539	11	B49114	protein-tyrosine kin	9.79e-11
20	158	35.9	557	1	TVFV82	protein-tyrosine kin	9.79e-11
21	158	35.9	568	1	TVFVS1	protein-tyrosine kin	9.79e-11
22	158	35.9	587	1	TVFVPR	protein-tyrosine kin	9.79e-11
23	157	35.7	451	12	S49016	tyrosine kinase - hu	1.40e-10
24	156	35.5	536	4	S33569	protein-tyrosine kin	1.99e-10
25	153	34.8	505	4	S24550	protein-tyrosine kin	5.73e-10
26	153	34.8	506	4	S24553	protein-tyrosine kin	5.73e-10
27	153	34.8	517	4	A43807	protein-tyrosine kin	5.73e-10
28	152	34.5	512	4	A39719	protein-tyrosine kin	8.14e-10
29	151	34.3	526	4	S20808	protein-tyrosine kin	1.16e-09
30	151	34.3	526	4	S15582	protein-tyrosine kin	1.16e-09
31	151	34.3	526	1	TVFVR	protein-tyrosine kin	1.16e-09
32	151	34.3	526	1	DKFVYR	protein-tyrosine kin	1.16e-09
33	147	33.4	505	1	TVHUHC	protein-tyrosine kin	4.68e-09
34	146	33.2	526	1	TVFV60	protein-tyrosine kin	6.62e-09
35	145	33.0	907	9	A57087	cell division contro	9.37e-09
36	144	32.7	503	1	TVMSHC	protein-tyrosine kin	1.32e-08
37	144	32.7	512	1	TVHUYL	protein-tyrosine kin	1.32e-08
38	143	32.5	526	7	S20676	protein-tyrosine kin	1.87e-08
39	143	32.5	526	7	S26420	src protein - Rous s	1.87e-08
40	142	32.3	503	4	J01321	protein-tyrosine kin	2.64e-08
41	140	31.8	545	7	S52313	pp62v protein - Rous	5.25e-08
42	140	31.8	546	7	S52314	pp62v protein - Rous	5.25e-08
43	131	29.8	303	5	S41754	CRKL protein - human	1.12e-06
44	130	29.5	259	5	A44988	transforming protein	1.56e-06
45	130	29.5	305	5	A49011	c-Crk - chicken	1.56e-06

## ALIGNMENTS

RESULT 1

ENTRY I38396 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human

ALTERNATE\_NAMES FYN-related kinase (FRK)

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 15-Mar-1996

ACCESSIONS I38396

REFERENCE I38396

#authors Lee, J.; Wang, Z.; Luch, S.M.; Wood, W.I.; Scadden, D.T.

#journal Gene (1994) 138:247-251

#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.

#cross-references MUID:94171047

#accession I38396

##status preliminary

##molecule\_type mRNA

##residues 1-505 ##label RES

##cross-references EMBL:U00803; NID:a392887; CDS PID:a392888

GENETICS  
#gene GDB:FRK  
##cross-references GDB:G00-355-675  
KEYWORDS phosphotransferase  
SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 95.9%; Score 422; DB 11; Length 505;  
Best Local Similarity 98.3%; Pred. No. 6.98e-56;  
Matches 58; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 49 alfdyqartaedlsfragdk-lqvldtlhegwwfarhlekkrrdgssqqlqgyipsnyva 106  
|||:|||||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 54 ALFDYQARTAEDLSFRAGDKKLVQLDTLHEGWWFARHLEKRRDGSSQQLQGYIPSNYVA 112

RESULT 2  
ENTRY TVHAST #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata  
ORGANISM #formal\_name Hydra attenuata  
DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change  
20-Aug-1994  
ACCESSIONS A34094  
REFERENCE A34094  
#authors Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.  
#journal Mol. Cell. Biol. (1989) 9:4141-4151  
#title Structure and expression of STK, a src-related gene in the  
simple metazoan Hydra attenuata.  
#cross-references MUID:90066418  
#accession A34094  
##molecule\_type mRNA  
##residues 1-509 ##label B05  
##cross-references GB:M25245  
GENETICS  
#gene stk  
CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
homology; SH2 homology; SH3 homology  
KEYWORDS ATP; phosphoprotein; phosphotransferase; transforming  
protein; tyrosine-specific protein kinase  
FEATURE  
66-115 #domain SH3 homology #label SH3\  
126-218 #domain SH2 homology #label SH2\  
238-497 #domain protein kinase homology #label KIN\  
246-254 #region protein kinase ATP-binding motif\  
268 #active\_site Lys #status predicted\  
390 #binding\_site phosphate (Tyr) (covalent) (by  
autophosphorylation) #status predicted  
SUMMARY #length 509 #molecular-weight 56885 #checksum 8721

Query Match 43.4%; Score 191; DB 1; Length 509;  
Best Local Similarity 47.7%; Pred. No. 6.03e-16;  
Matches 21; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Db 66 alydyearisedlsfkger-lqintadgdwwyarslitnseg 108  
||:||:|| :|||:| :||:||:||:||:||:||:||:||:||:||:  
Qy 54 ALFDYQARTAEDLSFRAGDKKLVQLDTLHEGWWFARHLEKRRDG 97

RESULT 3  
ENTRY B34104 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) src 2 - African clawed  
frog  
ALTERNATE\_NAMES kinase-related transforming protein (src); kinase-related  
transforming protein (src) 2  
ORGANISM #formal\_name Xenopus laevis #common\_name African clawed frog  
DATE 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change  
09-Sep-1994

ACCESSIONS B34104  
 REFERENCE A34104  
 #authors Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.  
 #journal J. Biol. Chem. (1989) 264:10649-10653  
 #title The two *Xenopus laevis* SRC genes are co-expressed and each produces functional pp(60src).  
 #cross-references MUID:89278134  
 #accession B34104  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type mRNA  
 ##residues 1-532 ##label STE  
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase  
 FEATURE  
 87-136 #domain SH3 homology ##label SH3\  
 147-244 #domain SH2 homology ##label SH2\  
 264-522 #domain protein kinase homology ##label KIN\  
 272-280 #region protein kinase ATP-binding motif  
 SUMMARY #length 532 #molecular-weight 59736 #checksum 7595

Query Match 38.6%; Score 170; DB 4; Length 532;  
 Best Local Similarity 50.0%; Pred. No. 1.33e-12;  
 Matches 19; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Db 87 alydyesrtetdlsfrkger-lqivnnntegdwwllarsl 123  
 ||:||:|| |||||| ||: ||::: ||:|| |  
 Gy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWWFARHL 91

RESULT 4  
 ENTRY A49114 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) fyn - Pacific electric ray  
 ORGANISM #formal\_name *Torpedo californica* #common\_name Pacific electric ray  
 DATE 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 19-Jan-1996  
 ACCESSIONS A49114  
 REFERENCE A49114  
 #authors Swope, S.L.; Huganir, R.L.  
 #journal J. Biol. Chem. (1993) 268:25152-25161  
 #title Molecular cloning of two abundant protein tyrosine kinases in *Torpedo* electric organ that associate with the acetylcholine receptor.  
 #accession A49114  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-542 ##label SWO  
 ##cross-references GB:U01349  
 CLASSIFICATION #superfamily protein kinase homology; SH3 homology  
 KEYWORDS phosphotransferase  
 FEATURE  
 94-143 #domain SH3 homology ##label SH3\  
 274-532 #domain protein kinase homology ##label KIN  
 SUMMARY #length 542 #molecular-weight 61096 #checksum 2657

Query Match 38.0%; Score 167; DB 11; Length 542;  
 Best Local Similarity 51.3%; Pred. No. 3.92e-12;  
 Matches 20; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Db 94 alydydarddddlsfhkgek-fqilnnntegdwwllarslq 131  
 ||:||:|| |||||| ||:|| :||:||: || || |:  
 Gy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWWFARHL 92

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 (TM)

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:55:24 1997; MasPar time 4.55 Seconds  
452,373 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-6  
Description: (122-201) from US08426509.pep (1 of 3)  
Perfect Score: 586  
Sequence: 1 WFFGAIGRSDAEKQLLYSEN.....FLTRRRIFSTLNEFVSHYTK 80

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 38.963; Variance 91.030; scale 0.428

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

4

Result	Query							
No.	Score	Match	Length	DB	ID	Description		Pred. No.
1	586	100.0	505	11	I38396	protein-tyrosine kin	4.99e-80	
2	351	59.9	499	4	A40092	protein-tyrosine kin	8.16e-40	
3	347	59.2	509	1	TVHAST	protein-tyrosine kin	3.78e-39	
4	344	58.7	506	4	S24553	protein-tyrosine kin	1.19e-38	
5	334	57.0	505	4	S24550	protein-tyrosine kin	5.45e-37	
6	333	56.8	505	11	S51647	protein-tyrosine kin	7.98e-37	
7	325	55.5	505	1	TVHUHC	protein-tyrosine kin	1.68e-35	
8	320	54.6	509	1	OKHULK	protein-tyrosine kin	1.12e-34	
9	319	54.4	503	4	JQ1321	protein-tyrosine kin	1.64e-34	
10	319	54.4	509	4	A23639	protein-tyrosine kin	1.64e-34	
11	316	53.9	503	1	TVMSHC	protein-tyrosine kin	5.11e-34	
12	310	52.9	512	1	TVHULY	protein-tyrosine kin	4.95e-33	
13	310	52.9	526	1	TVFV60	protein-tyrosine kin	4.95e-33	
14	310	52.9	533	1	TVCHS	protein-tyrosine kin	4.95e-33	
15	310	52.9	557	1	TVFV52	protein-tyrosine kin	4.95e-33	
16	310	52.9	568	1	TVFV51	protein-tyrosine kin	4.95e-33	
17	310	52.9	587	1	TVFVPR	protein-tyrosine kin	4.95e-33	
18	308	52.6	541	4	A43610	protein-tyrosine kin	1.05e-32	
19	308	52.6	542	1	TVHUSC	protein-tyrosine kin	1.05e-32	

20	307	52.4	512	4	A39719	protein-tyrosine kin	1.54e-32
21	303	51.7	523	1	TVFVMT	protein-tyrosine kin	6.94e-32
22	303	51.7	534	4	S33568	protein-tyrosine kin	6.94e-32
23	303	51.7	537	1	TVHUSY	protein-tyrosine kin	6.94e-32
24	303	51.7	545	7	S52313	pp62v protein - Rous	6.94e-32
25	303	51.7	546	7	S52314	pp62v protein - Rous	6.94e-32
26	302	51.5	537	1	TVHUSR	protein-tyrosine kin	1.01e-31
27	300	51.2	534	4	A44991	protein-tyrosine kin	2.15e-31
28	299	51.0	537	4	A43806	protein-tyrosine kin	3.13e-31
29	299	51.0	541	12	S31645	protein-tyrosine kin	3.13e-31
30	299	51.0	663	1	TVMVRR	protein-tyrosine kin	3.13e-31
31	298	50.9	529	1	TVHUF	protein-tyrosine kin	4.55e-31
32	297	50.7	536	4	S33569	protein-tyrosine kin	6.63e-31
33	297	50.7	537	4	A45501	protein-tyrosine kin	6.63e-31
34	297	50.7	543	1	TVHUY	protein-tyrosine kin	6.63e-31
35	296	50.5	517	4	A43807	protein-tyrosine kin	9.66e-31
36	296	50.5	539	11	B49114	protein-tyrosine kin	9.66e-31
37	292	49.8	392	4	S04205	protein-tyrosine kin	4.33e-30
38	292	49.8	542	11	A49114	protein-tyrosine kin	4.33e-30
39	290	49.5	362	4	S24551	protein-tyrosine kin	9.16e-30
40	290	49.5	528	1	TVFVG	protein-tyrosine kin	9.16e-30
41	290	49.5	541	1	TVCHYS	protein-tyrosine kin	9.16e-30
42	289	49.3	532	4	B34104	protein-tyrosine kin	1.33e-29
43	288	49.1	507	4	A39939	protein-tyrosine kin	1.94e-29
44	288	49.1	517	12	S24547	protein-tyrosine kin	1.94e-29
45	288	49.1	532	4	A34104	protein-tyrosine kin	1.94e-29

## ALIGNMENTS

RESULT 1

ENTRY I38396 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human

ALTERNATE\_NAMES FYN-related kinase (FRK)

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 15-Mar-1996

ACCESSIONS I38396

REFERENCE I38396

#authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.

#journal Gene (1994) 138:247-251

#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.

#cross-references MUID:94171047

#accession I38396

##status preliminary

##molecule\_type mRNA

##residues 1-505 ##label RES

##cross-references EMBL:U00803; NID:g392887; CDS\_PID:g392888

GENETICS

#gene GDB:FRK.

#cross-references GDB:G00-355-675

KEYWORDS phosphotransferase

SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 100.0%; Score 586; DB 11; Length 505;  
 Best Local Similarity 100.0%; Pred. No. 4.99e-80;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 wffgaigrsdaekqllysenktgsfliresesqkgefslsvldgavvkhryikrldeggf 175

||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Gy 122 WFFGAIGRSDAEKQLLYSENKTGSFLIRESESQKGEFSLSVLDGAVVKHRYIKRLDEGGF 181

Db 176 fltrrrrifstlnefvshytk 195

||||||||||||||||||||

Gy 182 FLTRRRIFSTLNNEFVSHYTK 201

RESULT 2

ENTRY A40092 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) blk - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change  
09-Sep-1994

ACCESSIONS A40092

REFERENCE A40092

#authors Dynicki, S.M.; Niederhuber, J.E.; Desiderio, S.V.

#journal Science (1990) 247:332-336

#title Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.

#cross-references MUID:90117147

#accession A40092

##status preliminary

##molecule\_type mRNA

##residues 1-499 ##label DYM

##cross-references GB:M30903

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE

59-107 #domain SH3 homology ##label SH3\

118-214 #domain SH2 homology ##label SH2\

233-491 #domain protein kinase homology ##label KIN\

241-249 #region protein kinase ATP-binding motif

SUMMARY #length 499 #molecular-weight 56644 #checksum 4536

Query Match 59.9%; Score 351; DB 4; Length 499;  
Best Local Similarity 58.3%; Pred. No. 8.16e-40;  
Matches 49; Conservative 17; Mismatches 14; Indels 4; Gaps 2;

Db 118 wffrtisrkdaerqllapankagsfliresesnkafslsvkdittqgevvkhykirsld 177  
||| :||| ||||:||| : ||:|||||||||| || |||| : :| ||||:||| :|||  
Qy 122 WFFGAIGRSDAEKOLLYSENKTGSFLIRESESQKGEFSLSV--L--DGAVVKHYRIKRLD 177

Db 178 ngggyyisprifptlqalvqhysk 201  
:||:||:| | :||| :| ||:|  
Qy 178 EGGFFLTRRRIFSTLNEFVSHYTK 201

RESULT 3

ENTRY TVHAST #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata

ORGANISM #formal\_name Hydra attenuata

DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change  
20-Aug-1994

ACCESSIONS A34094

REFERENCE A34094

#authors Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.

#journal Mol. Cell. Biol. (1989) 9:4141-4151

#title Structure and expression of STK, a src-related gene in the simple metazoan Hydra attenuata.

#cross-references MUID:90066418

#accession A34094

##molecule\_type mRNA

##residues 1-509 ##label BOS

##cross-references GB:M25245

GENETICS

#gene stk

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific protein kinase

59 Sequence 3898 AA;

Query Match 45.9%; Score 51; DB 17; Length 3898;  
Best Local Similarity 33.3%; Pred. No. 1.94e+02;  
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0

Db 3144 hlvgdiatikekakq 3158  
      :|: | :|| |:  
Qu 661 QLLSSIEPLREKDKH 675

Search completed: Mon Feb 3 17:08:40 1997

Job time : 10 secs.

\*\*\*\*\*

MAP MAP MAP MAP

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:08:03 1997; MasPar time 2.69 Seconds  
153.247 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
Description: (660-675) from US08426509.pep (5 of 5  
Perfect Score: 111  
Sequence: I QQLLSSIEPLREKDKH 16

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

**Post-processing: Minimum Match 0%**  
**Listing first 45 summaries**

Database: pir48  
1:anni 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann10  
14:unrev

Statistics: Mean 27.034; Variance 49.322; scale 0.548

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

7

Result		Query					
No.	Score	Match	Length	DB	ID	Description	Pred. No
1	68	61 3	148	11	S31791	statmin - chicken	8.00e-01

2	68	61.3	149	5	A40936	stathmin - human	8.00e-01
3	68	61.3	149	12	B48917	stathmin - mouse	8.00e-01
4	68	61.3	149	5	A34294	stathmin - rat	8.00e-01
5	68	61.3	197	7	J01271	hypothetical 21.5K p	8.00e-01
6	65	58.6	1009	9	S61174	hypothetical protein	2.28e+00
7	62	55.9	678	10	S56284	hypothetical protein	6.30e+00
8	61	55.0	993	12	S49461	synaptonemal complex	8.79e+00
9	61	55.0	993	12	S59599	synaptonemal complex	8.79e+00
10	60	54.1	192	14	JC4573	Ras2 protein - Hydra	1.22e+01
11	60	54.1	192	10	S32042	RAS1 protein - Hydra	1.22e+01
12	59	53.2	805	1	YUP05	sucrose synthase (EC	1.70e+01
13	58	52.3	243	8	S42873	probable succinate d	2.34e+01
14	58	52.3	605	3	ABPGS	serum albumin precur	2.34e+01
15	58	52.3	681	6	A36500	transferrin precurso	2.34e+01
16	58	52.3	2470	9	S57085	1-phosphatidylinosit	2.34e+01
17	57	51.4	437	11	S15704	transforming protein	3.22e+01
18	57	51.4	708	9	S53411	hypothetical protein	3.22e+01
19	57	51.4	763	6	S55616	glycoprotein H - equ	3.22e+01
20	56	50.5	179	12	A48917	SCG10 protein - mous	4.42e+01
21	56	50.5	179	5	A36110	SCG10 protein - rat	4.42e+01
22	56	50.5	237	7	JH0671	high-affinity branch	4.42e+01
23	56	50.5	239	7	JC4346	flagellar-specific s	4.42e+01
24	56	50.5	241	7	S47673	leucine transport pr	4.42e+01
25	56	50.5	494	1	B45738	alpha-amylase (EC 3.	4.42e+01
26	56	50.5	495	1	A45738	alpha-amylase (EC 3.	4.42e+01
27	56	50.5	508	9	S19697	aspartic proteinase	4.42e+01
28	56	50.5	598	3	RGECNX	regulatory protein n	4.42e+01
29	56	50.5	660	12	A53618	regulatory protein N	4.42e+01
30	56	50.5	756	8	B64137	tetrahydropteroyltri	4.42e+01
31	56	50.5	808	4	S25526	sucrose synthase (EC	4.42e+01
32	56	50.5	808	4	S23543	sucrose synthase (EC	4.42e+01
33	56	50.5	985	10	A32240	REVI protein - yeast	4.42e+01
34	56	50.5	1581	11	S49149	laminin A3 - human	4.42e+01
35	55	49.5	238	10	S22609	hypothetical protein	6.03e+01
36	55	49.5	373	7	S15200	hydrogenase isozyme	6.03e+01
37	55	49.5	406	8	S38218	hypothetical protein	6.03e+01
38	55	49.5	407	4	A49845	5-aminolevulinate sy	6.03e+01
39	55	49.5	607	3	ABB05	serum albumin precur	6.03e+01
40	55	49.5	607	3	ABSH5	serum albumin precur	6.03e+01
41	55	49.5	807	4	S29242	sucrose synthase (EC	6.03e+01
42	54	48.6	406	12	S27010	aminoacylase (EC 3.5	8.21e+01
43	54	48.6	802	1	YUZMS	sucrose synthase (EC	8.21e+01
44	54	48.6	1025	4	JC1266	beta-galactosidase (	8.21e+01
45	54	48.6	2016	10	S27411	cell division-associ	8.21e+01

## ALIGNMENTS

RESULT 1

ENTRY S31791 #type complete

TITLE stathmin - chicken

ORGANISM #formal\_name Gallus gallus #common\_name chicken

DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change  
13-Jan-1995

ACCESSIONS S31791

REFERENCE S20720

#authors Godbout, R.

#submission submitted to the EMBL Data Library, April 1992

#description Identification and characterization of transcripts present at elevated levels in the undifferentiated chick retina.

#accession S31791

#status preliminary

#molecule\_type mRNA

#residues 1-148 #label GOD

#cross-references EMBL:X67840

SUMMARY #length 148 #molecular-weight 17082 #checksum 8231

Query Match 61.3%; Score 68; DB 11; Length 148;  
Best Local Similarity 60.0%; Pred. No. 8.00e-01;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qmaaklerlrekdkh 129

||: : :| |||||

Gy 661 QLLSSIEPLREKDKH 675

RESULT 2

ENTRY A40936 #type complete  
TITLE stathmin - human  
ALTERNATE\_NAMES leukemia-associated phosphoprotein p18; oncoprotein 18; Pr22 protein; proliferation-related phosphoprotein p18  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 28-May-1992 #sequence\_revision 28-May-1992 #text\_change 01-Mar-1996  
ACCESSIONS A40936; A44780; S31624; S10565; A39215; S42211  
REFERENCE A40936  
#authors Melhem, R.F.; Zhu, X.; Hailat, N.; Strahler, J.R.; Hanash, S.M.  
#journal J. Biol. Chem. (1991) 266:17747-17753  
#title Characterization of the gene for a proliferation-related phosphoprotein (oncoprotein 18) expressed in high amounts in acute leukemia.  
#cross-references MUID:92011487  
#accession A40936  
##molecule\_type DNA  
##residues 1-149 ##label MEL  
##cross-references GB:M31303  
REFERENCE A44780  
#authors Zhu, X.; Kozarsky, K.; Strahler, J.R.; Eckerskorn, C.; Lottspeich, F.; Melhem, R.; Lowe, J.; Fox, D.A.; Hanash, S.M.; Atweh, G.F.  
#journal J. Biol. Chem. (1989) 264:14556-14560  
#title Molecular cloning of a novel human leukemia-associated gene. Evidence of conservation in animal species.  
#accession A44780  
##molecule\_type mRNA  
##residues 1-149 ##label ZHU  
##cross-references GB:J04991  
REFERENCE S31624  
#authors Marunouchi, T.  
#submission submitted to the EMBL Data Library, January 1992  
#accession S31624  
##status preliminary  
##molecule\_type mRNA  
##residues 1-149 ##label MAR  
##cross-references EMBL:Z11566  
REFERENCE S10565  
#authors Maucuer, A.; Doye, V.; Sobel, A.  
#journal FEBS Lett. (1990) 244:275-278  
#title A single amino acid difference distinguishes the human and the rat sequences of stathmin, a ubiquitous intracellular phosphoprotein associated with cell regulations.  
#cross-references MUID:90292224  
#accession S10565  
##status preliminary  
##molecule\_type mRNA  
##residues 1-149 ##label MAU  
REFERENCE A39215  
#authors Gullberg, M.; Noreus, K.; Brattsand, G.; Friedrich, B.; Shingler, V.  
#journal J. Biol. Chem. (1990) 265:17499-17505  
#title Purification and characterization of a 19-kilodalton

intracellular protein. An activation-regulated putative protein kinase C substrate of T lymphocytes.

#cross-references MUID:91009201

#accession A39215

##molecule\_type protein

##residues 117-136 ##label GUL

REFERENCE S42211

#authors Brattsand, G.; Marklund, U.; Nylander, K.; Roos, G.; Gullberg, M.

#journal Eur. J. Biochem. (1994) 220:359-368

#title Cell-cycle-regulated phosphorylation of oncoprotein 18 on Ser16, Ser25 and Ser38.

#accession S42211

##status preliminary

##molecule\_type protein

##residues 11-44 ##label BRA

GENETICS

#gene GDB:LAP18

##cross-references GDB:G00-127-971

#map\_position 1p36.1-p35

CLASSIFICATION #superfamily stathmin

KEYWORDS cytosol; phosphoprotein

FEATURE

16,25,38 #binding\_site phosphate (Ser) (covalent) #status experimental

SUMMARY #length 149 #molecular-weight 17302 #checksum 1901

Query Match 61.3%; Score 68; DB 5; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qmaaklerlrekdkh 129

||: : :| |||||||

Qy 661 QLLSSIEPLREKDKH 675

RESULT 3

ENTRY B48917 #type complete

TITLE stathmin - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 01-Dec-1995

ACCESSIONS B48917

REFERENCE A48917

#authors Okazaki, T.; Yoshida, B.N.; Avraham, K.B.; Wang, H.; Wuenschell, C.W.; Jenkins, N.A.; Copeland, N.G.; Anderson, D.J.; Mori, N.

#journal Genomics (1993) 18:360-373

#title Molecular diversity of the SCG10/stathmin gene family in the mouse.

#accession B48917

##status preliminary

##molecule\_type DNA

##residues 1-149 ##label OKA

##cross-references GB:L20258

##note authors translated the codon GAT for residue 34 as Glu

SUMMARY #length 149 #molecular-weight 17274 #checksum 2075

Query Match 61.3%; Score 68; DB 12; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qmaaklerlrekdkh 129

||: : :| |||||||

Qy 661 QLLSSIEPLREKDKH 675

RESULT 4

ENTRY A34294 #type complete

TITLE stathmin - rat

ALTERNATE\_NAMES phosphoprotein p19

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change  
18-Jun-1993

ACCESSIONS A34294; A32892

REFERENCE A34294

#authors Doye, V.; Soubrier, F.; Bauw, G.; Bouterin, M.C.; Beretta, L.; Koppel, J.; Vandekerckhove, J.; Sobel, A.

#journal J. Biol. Chem. (1989) 264:12134-12137

#title A single cDNA encodes two isoforms of stathmin, a developmentally regulated neuron-enriched phosphoprotein.

#cross-references MUID:89308626

#accession A34294

##molecule\_type mRNA

##residues 1-149 ##label D0Y

##cross-references GB:J04979

REFERENCE A32892

#authors Schubart, U.K.; Banerjee, M.D.; Eng, J.

#journal DNA (1989) 8:389-398

#title Homology between the cDNAs encoding phosphoprotein p19 and SCG10 reveals a novel mammalian gene family preferentially expressed in developing brain.

#cross-references MUID:89377477

#accession A32892

##molecule\_type mRNA

##residues 1-149 ##label SCH

##cross-references GB:M27876

CLASSIFICATION #superfamily stathmin

SUMMARY #length 149 #molecular-weight 17288 #checksum 2109

Query Match 61.3%; Score 68; DB 5; Length 149;  
Best Local Similarity 60.0%; Pred. No. 8.00e-01;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qmaaklerlrekdkh 129  
|: : :| |||||||  
Qy 661 QLLSSIEPLREKDKH 675

RESULT 5

ENTRY JQ1271 #type complete

TITLE hypothetical 21.5K protein - Escherichia coli

ALTERNATE\_NAMES ORFE protein

ORGANISM #formal\_name Escherichia coli

DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change  
27-Jan-1995

ACCESSIONS JQ1271; S24198

REFERENCE JQ1271

#authors Wachi, M.; Doi, M.; Ueda, T.; Ueki, M.; Tsuritani, K.; Nagai, K.; Matsuhashi, M.

#journal Gene (1991) 106:135-136

#title Sequence of the downstream flanking region of the shape-determining genes *mreBCD* of *Escherichia coli*.

#cross-references MUID:92039056

#accession JQ1271

##molecule\_type DNA

##residues 1-197 ##label WAC

##cross-references EMBL:X57166

COMMENT The gene encoding for this protein is located at downstream of the *mre* genes.

SUMMARY #length 197 #molecular-weight 21515 #checksum 3123

\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:06:00 1997; MasPar time 9.04 Seconds  
 671.741 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
 Description: (424-659) from US08426509.pep (4 of 5)  
 Perfect Score: 1845  
 Sequence: 1 CSGQFGVYVQLGKWKGQYDVA.....TIYGIMYSCWHELPEKRPTF 236

Scoring table: PAM 150  
 Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: pir48  
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
 14:unrev

Statistics: Mean 43.995; Variance 98.402; scale 0.447

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
--------	-------	-----	-------	-------	--------	----	----	-------------	-----------

1	1327	71.9	659	11	I37212			Bruton agammaglobuli	2.40e-218
2	1327	71.9	659	11	S28912			protein-tyrosine kin	2.40e-218
3	1299	70.4	660	12	JN0471			protein-tyrosine kin	4.41e-213
4	1288	69.8	659	12	B45184			B cell progenitor ki	5.15e-211
5	1255	68.0	527	12	A55631			protein-tyrosine kin	8.12e-205
6	1223	66.3	527	4	S13763			protein-tyrosine kin	8.20e-199
7	1207	65.4	608	4	JU0227			protein-tyrosine kin	8.20e-196
8	1207	65.4	630	4	JU0228			protein tyrosine kin	8.20e-196
9	1188	64.4	602	4	JU0215			tyrosine kinase, tec	2.98e-192
10	1168	63.3	620	4	S33253			protein-tyrosine kin	1.66e-188
11	1157	62.7	619	4	A47333			T-cell-specific tyro	1.91e-186
12	1157	62.7	625	4	A43030			protein-tyrosine kin	1.91e-186
13	1129	61.2	619	4	JN0472			protein-tyrosine kin	3.30e-181
14	1117	60.5	590	1	TVFFDS			protein-tyrosine kin	5.79e-179
15	915	49.6	506	4	S24553			protein-tyrosine kin	2.35e-141
16	860	46.6	362	4	S24551			protein-tyrosine kin	3.54e-131
17	858	46.5	1520	1	TVFFA			protein-tyrosine kin	8.29e-131
18	847	45.9	507	4	A39939			protein-tyrosine kin	8.92e-129
19	844	45.7	505	4	S24550			protein-tyrosine kin	3.19e-128
20	836	45.3	509	4	A23639			protein-tyrosine kin	9.56e-127
21	835	45.3	509	1	OKHULK			protein-tyrosine kin	1.46e-126
22	826	44.8	509	1	TVHAST			protein-tyrosine kin	6.68e-125
23	824	44.7	308	1	TVFFS			protein-tyrosine kin	1.56e-124

24	823	44.6	542	11	A49114	protein-tyrosine kin	2.39e-124
25	821	44.5	557	10	A00629	protein-tyrosine kin	5.58e-124
26	819	44.4	334	4	S24552	protein-tyrosine kin	1.30e-123
27	820	44.4	697	7	A26132	gag-abl-pol polyprot	8.53e-124
28	817	44.3	1130	1	TVHUA	protein-tyrosine kin	3.05e-123
29	815	44.2	537	4	A43806	protein-tyrosine kin	7.12e-123
30	815	44.2	981	1	F0MVGM	gag-abl polyprotein	7.12e-123
31	815	44.2	1123	4	A39962	kinase-related trans	7.12e-123
32	812	44.0	537	1	TVHUSY	protein-tyrosine kin	2.54e-122
33	809	43.8	505	11	S51647	protein-tyrosine kin	9.07e-122
34	808	43.8	537	1	TVHUSR	protein-tyrosine kin	1.39e-121
35	802	43.5	539	11	B49114	protein-tyrosine kin	1.76e-120
36	800	43.4	536	4	S33569	protein-tyrosine kin	4.12e-120
37	798	43.3	568	1	TVFVSI	protein-tyrosine kin	9.61e-120
38	799	43.3	1146	4	B35962	protein-tyrosine kin	6.29e-120
39	799	43.3	1182	4	A35962	protein-tyrosine kin	6.29e-120
40	797	43.2	526	1	TVFV60	protein-tyrosine kin	1.47e-119
41	797	43.2	532	4	A34104	protein-tyrosine kin	1.47e-119
42	797	43.2	532	4	B34104	protein-tyrosine kin	1.47e-119
43	796	43.1	505	11	I38396	protein-tyrosine kin	2.24e-119
44	796	43.1	541	4	A43610	protein-tyrosine kin	2.24e-119
45	796	43.1	542	1	TVHUSC	protein-tyrosine kin	2.24e-119

### ALIGNMENTS

RESULT 1

ENTRY I37212 #type complete

TITLE Bruton agammaglobulinemia tyrosine kinase - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Mar-1996

ACCESSIONS I37212

REFERENCE I37212

#authors Ohta, Y.; Haire, R.N.; Litman, R.T.; Fu, S.M.; Nelson, R.P.; Kratz, J.; Kornfeld, S.J.; de la Morena, M.; Good, R.A.; Litman, G.W.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9062-9066

#title Genomic organization and structure of Bruton agammaglobulinemia tyrosine kinase: localization of mutations associated with varied clinical presentations and course in X chromosome-linked agammaglobulinemia.

#cross-references MUID:94377492

#accession I37212

##status preliminary

##molecule\_type DNA

##residues 1-659 ##label RES

##cross-references EMBL:U10087; NID:g517436; CDS\_PID:g517438

##note only intron-exon junctions are shown

GENETICS

#gene GDB:BTK; AGMX1; IMD1

##cross-references GDB:G00-120-542

#map\_position Xq21.33-q22

#introns 47/3; 80/3; 103/3; 131/1; 174/1; 196/3; 259/2; 280/2; 298/3; 325/2; 368/1; 393/1; 450/2; 522/3; 544/2; 584/1; 636/3

SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 71.9%; Score 1327; DB 11; Length 659;  
 Best Local Similarity 67.8%; Pred. No. 2.40e-218;  
 Matches 160; Conservative 41; Mismatches 35; Indels 0; Gaps 0;

Db 409 gtgqfgvvkygkurgqydvaikmikegsmsedefieeakvmmnlsheklvqlgyvctkqr 468  
 ||||||| ||||:|||||:||||||||||:||| ||:||| ||| :||||:|:

Gy 424 GSG@FGVVQLGKWKCG@YDVAVKMIKEGSMSEDEFF@EAGTMMKLSHPKLVKFYGVCSKEY 483

Db 469 pifiiteymangcllnulremrhrfqtgallemckdvceameuleskqflhrdlaarncl 528

||:||||:||||:||||:|| :: |||||| ||||:| :||| ||:||||:||||  
Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLLEM CYDVC EGM AFLE SHQFI HRDLA ARNCL 543  
Db 529 vndqg vvk v s d f g l s r y v l d d e y t s s v g s k f p v r u s p p e v l m y s k f s s k s d i w a f g v l m w 588  
||: : ||||||:||:||||:|| :|||:|||:||:|||:|| :|||:|||:|||:|||:|||  
Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGT KFPVKW S A P E V F H Y F K Y S S K S D V W A F G I L M W 603  
Db 589 e i y s l g k m p y e r f t n s e a h i a q g l r l y r p h l a s e k v y t i m y s c u h e k a d e r p t f 644  
||:|||| ||: : ||: :||| ||||||:||:|||:|||:|||:|||:|||:|||  
Qy 604 EVFSLGK QPYDLYD NSQVVLKVS QGHRLYRPHLASDTIYQIMYSCHWELPEKRPTF 659

RESULT 2  
ENTRY S28912 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) atk - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change  
01-Dec-1995  
ACCESSIONS S28912  
REFERENCE S28912  
#authors Vetric, D.; Vorechovsky, I.; Sideras, P.; Holland, J.;  
Davies, A.; Flinter, F.; Hammarstrom, L.; Kinnon, C.;  
Levinsky, R.; Bobrow, M.; Smith, C.I.E.; Bentley, D.R.  
#journal Nature (1993) 361:226-233  
#title The gene involved in X-linked agammaglobulinaemia is a member  
of the src family of protein-tyrosine kinases.  
#accession S28912  
##status preliminary  
##molecule\_type mRNA  
##residues 1-659 ##label VET  
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
homology  
KEYWORDS phosphotransferase  
FEATURE  
221-269 #domain SH3 homology #label SH3\  
281-377 #domain SH2 homology #label SH2\  
400-658 #domain protein kinase homology #label KIN  
SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 71.9%; Score 1327; DB 11; Length 659;  
Best Local Similarity 67.8%; Pred. No. 2.40e-218;  
Matches 160; Conservative 41; Mismatches 35; Indels 0; Gaps 0;

Db 409 gtgqfgvvkygkurgqydvaikmikegsnsedefieeakvmmnlsheklvqlygvctkqr 468  
||:|||| ||:||||:||:||||:||:|||:|||:|||:|||:|||:|||:|||  
Qy 424 GSGQFGVVYQLGKWKGGYDVAVKMIKEGSMSEDEF FQEAQGTMMKL SHPKLVKFYGVCSKEY 483  
Db 469 pifiiteymangcllnylremhrfqtqqlle mckd vceameyleskqflhrdlaarncl 528  
|||:||:||:||:||:||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLLEM CYDVC EGM AFLE SHQFI HRDLA ARNCL 543  
Db 529 vndqg vvk v s d f g l s r y v l d d e y t s s v g s k f p v r u s p p e v l m y s k f s s k s d i w a f g v l m w 588  
||: : ||||||:||:||||:|| :|||:|||:||:|||:|||:|||:|||  
Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGT KFPVKW S A P E V F H Y F K Y S S K S D V W A F G I L M W 603  
Db 589 e i y s l g k m p y e r f t n s e a h i a q g l r l y r p h l a s e k v y t i m y s c u h e k a d e r p t f 644  
||:|||| ||: : ||: :||| ||||||:||:|||:|||:|||:|||  
Qy 604 EVFSLGK QPYDLYD NSQVVLKVS QGHRLYRPHLASDTIYQIMYSCHWELPEKRPTF 659

RESULT 3  
ENTRY JN0471 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) emb - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change  
12-May-1995

ACCESSIONS JN0471  
 REFERENCE JN0471  
 #authors Yamada, N.; Kawakami, Y.; Kimura, H.; Fukamachi, H.; Baier, G.; Altman, A.; Kato, T.; Inagaki, Y.; Kawakami, T.  
 #journal Biochem. Biophys. Res. Commun. (1993) 192:231-240  
 #title Structure and expression of novel protein-tyrosine kinases, Emb and Emt, in the hematopoietic cells.  
 #accession JN0471  
 ##molecule\_type mRNA  
 ##residues 1-660 ##label YAM  
 ##note the nucleotide sequence is not given  
**GENETICS**  
 #gene emb  
**CLASSIFICATION** #superfamily SH3 homology; protein kinase homology; SH2 homology  
**KEYWORDS** phosphotransferase  
**FEATURE**  
 223-271 #domain SH3 homology #label SH3  
 283-379 #domain SH2 homology #label SH2  
 402-659 #domain protein kinase homology #label KIN  
 552 #binding\_site phosphate (Tyr) (covalent) #status predicted  
**SUMMARY** #length 660 #molecular-weight 76577 #checksum 1680

Query Match 70.4%; Score 1299; DB 12; Length 660;  
 Best Local Similarity 66.5%; Pred. No. 4.41e-213;  
 Matches 157; Conservative 44; Mismatches 34; Indels 1; Gaps 1;

Db	411	gtgqfgvvkygkurgqydvaikmiregsasedefieeak-vnnlsheklvqllygvctkqr 469
Qy	424	GSGQFGVVQLGKWKGGYDVAVKMIKEGSMSEDEFFQEAGTMMKLSHPKLVKFYGVCSKEY 483
Db	470	pifiiteymangcllnylremrhrfqtqqllmekdvceameyleskqflhrdlaarncl 529
Qy	484	PIYIVTEYISNGCLLNYLRSHGKGLEPSQLLEMCDVCEGMAFLESHQFIHRDLAARNCL 543
Db	530	vndqgvvksdfglrsryvlddeytssvgskfpvrwsppevlmyskfsksdiwafgvlmw 589
Qy	544	VDRDLCVKVSDFGMTRYVLDDQYVSSVGTKFPVKNSAPEVFHYFKYSSKSDVWAFGILMW 603
Db	590	eiyslgkmpyerftnsetaechiaqglrllyrphlaservytimyscuhekaderpsf 645
Qy	604	EVFSLGKQPYDLYDNGQVVLKVSQGHRLYRPHLASDTIYQIMYSCHWELPEKRPTF 659

**RESULT** 4  
**ENTRY** B45184 #type complete  
**TITLE** B cell progenitor kinase, BPK=cytoplasmic tyrosine kinase - mouse  
**ORGANISM** #formal\_name Mus musculus #common\_name house mouse  
**DATE** 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 12-May-1995  
**ACCESSIONS** B45184  
**REFERENCE** A45184  
 #authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.; Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.; Mohandas, T.; Quan, S.; Belmont, J.W.; Cooper, M.D.; Conley, M.E.; Witte, O.N.  
 #journal Cell (1993) 72:279-290  
 #title Deficient expression of a B cell cytoplasmic tyrosine kinase in human X-linked agammaglobulinemia.  
 #cross-references MUID:93145329  
 #accession B45184  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type nucleic acid  
 ##residues 1-659 ##label TSU

##cross-references NCBIP:123834  
 ##experimental\_source 70z/3 pre-B cell line  
 ##note sequence extracted from NCBI backbone  
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2 homology  
 FEATURE  
 221-269 #domain SH3 homology #label SH3\  
 281-377 #domain SH2 homology #label SH2\  
 400-658 #domain protein kinase homology #label KIN  
 SUMMARY #length 659 #molecular-weight 76326 #checksum 9917

Query Match 69.8%; Score 1288; DB 12; Length 659;  
 Best Local Similarity 66.1%; Pred. No. 5.15e-211;  
 Matches 156; Conservative 43; Mismatches 37; Indels 0; Gaps 0;  
  
 Db 409 gtgqfgvvkygkurgqydvaikmiregsmseedfieeakvmmnlsheklvqlygvctkqr 468  
 ||:||||| ||||:||||||:||:||||||||:||| ||:||| ||| :||||:|||  
 Qy 424 GSGQFGVVVQLGKWKGGYDVAVKMIKEGSMSEDEFFQEAGTMMKLSHPKLVKFYGVCSKEY 483  
  
 Db 469 pifiiteymangcllnylremrhrfqtqqllemckdvceameyleskqflhrdlaarncl 528  
 ||:|:||:||:||||||| :: ||||||| ||||:| :||| ||:|||||||  
 Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLLEMCDVCEGMAFLESHQFIHRDLAARNCL 543  
  
 Db 529 vndqgvvkvslpglsryvlddeytssvgskfpvrwsppevlayskfsksdiwafgvlmw 588  
 ||: : ||||| |:||:||||||| ||||:||||:|||:|||: | :|||:||:||||:|||  
 Qy 544 VDRDLCVKVSDFGMTRYVLDDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603  
  
 Db 589 eiyslgkmpyerftnsetaehtiaqglrllyrphlaservytimyscuhekaderpsf 644  
 ||:||||| ||: : ||: ::||| |||||||||: :| ||||||||| :: ||:|||  
 Qy 604 EVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCHWELPEKRPTF 659

RESULT 5  
 ENTRY A55631 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) rlk - mouse  
 ALTERNATE\_NAMES resting lymphocyte kinase  
 ORGANISM #formal\_name Mus sp. #common\_name mouse  
 DATE 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change  
 12-May-1995  
 ACCESSIONS A55631  
 REFERENCE A55631  
 #authors Hu, Q.; Davidson, D.; Schwartzberg, P.L.; Macchiarini, F.;  
 Lenardo, M.J.; Bluestone, J.A.; Matis, L.A.  
 #journal J. Biol. Chem. (1995) 270:1928-1934  
 #title Identification of rlk, a novel protein tyrosine kinase with  
 predominant expression in the T cell lineage.  
 #accession A55631  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-527 #label HUA  
 ##cross-references GB:L35268  
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology  
 KEYWORDS phosphotransferase  
 FEATURE  
 89-137 #domain SH3 homology #label SH3\  
 269-527 #domain protein kinase homology #label KIN  
 SUMMARY #length 527 #molecular-weight 61108 #checksum 785

Query Match 68.0%; Score 1255; DB 12; Length 527;  
 Best Local Similarity 65.5%; Pred. No. 8.12e-205;  
 Matches 156; Conservative 40; Mismatches 38; Indels 4; Gaps 4;  
  
 Db 278 gsgqfgvvhlgewrahipvaikaineqsmseedfieeakvmmklshsrlvqlygvciqqk 337  
 ||||||||:|| |::: ||:| ||||||||:||:||| ||||||||:|| :||| :  
 Qy 424 GSGQFGVVVQLGKWKGGYDVAVKMIKEGSMSEDEFFQEAGTMMKLSHPKLVKFYGVCSKEY 483

RESULT 6

ENTRY S13763 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) tec - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 08-Dec-1995

ACCESSIONS S13763

REFERENCE S13763

#authors Mano, H.; Ishikawa, F.; Nishida, J.; Hirai, H.; Takaku, F.

#journal Oncogene (1990) 5:1781-1786

#title A novel protein-tyrosine kinase, tec, is preferentially expressed in liver.

#cross-references MUID:91133729

#accession S13763

##molecule\_type mRNA

##residues 1-527 ##label MAN

##cross-references EMBL:X55663

GENETICS

#gene tec

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE

104-142 #domain SH3 homology #status atypical #label SH3\

264-522 #domain protein kinase homology #label KIN

SUMMARY #length 527 #molecular-weight 61556 #checksum 5620

Query Match 66.3%; Score 1223; DB 4; Length 527;  
Best Local Similarity 61.0%; Pred. No. 8.20e-199;  
Matches 144; Conservative 45; Mismatches 47; Indels 0; Gaps 0

RESULT 7  
ENTRY JU0227 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) tec III - mouse  
ORGANISM #formal\_name *Mus musculus* #common\_name house mouse  
DATE 31-Dec-1993 #sequence revision 31-Dec-1993 #text change